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Perfect score:
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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1371.902 Million cell updates/sec
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    /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compug
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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US-10-001-189-46
US-10-001-189-53
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                                                                                                                                                     Sequence 40, Appl
Sequence 41, Appl
Sequence 46, Appl
Sequence 53, Appl
Sequence 55, Appl
Sequence 56, Appl
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Sequence 5863, Ap
Sequence 3188, Ap
Sequence 780, App
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Sequence 1,
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| 25 | 25 | 25 | 25 | 25.2 | 25.2 | 25.2 | 25.2 | 25.4 | 25.4 | 25.4 | 25.4 | 25.4 | 25.4 | 25.4 | 25.6 | 25.6 | 26 | 26.4 | 26.6 | 26.6 | 26.6 | 26.6 | 26.8 | 26.8 | 26.8 |
| 25.0 | 25.0 | 25.0 | 25.0 | 25.2 | 25.2 | 25.2 | 25.2 | 25.4 | 25.4 | 25.4 | 25.4 | 25.4 | 25.4 | 25.4 | 25.6 | 25.6 | 26.0 | 26.4 | 26.6 | 26.6 | 26.6 | 26.6 | 26.8 | 26.8 | 26.8 |
| 1837 | 1461 | 576 | 488 | 1668 | 589 | 405 | 233 | 4550 | 4550 | 1381 | 1381 | 1381 | 1381 | 286 | 2264 | 449 | 1491 | 4440 | 2002 | 783 | 783 | 783 | 4821 | 4550 | 3177 |
| 10 | 10 | 9 | 10 | 9 | 10 | 9 | 10 | 10 | 9 | 10 | 10 | 9 | 9 | 10 | 9 | 10 | 10 | 10 | 10 | 12 | 9 | 9 | 10 | 10 | 10 |
| US-09-925-301-365 | US-09-759-990-1 | US-09-764-868-523 | US-09-833-381-1066 | US-09-738-626-2694 | US-09-864-761-7274 | US-10-040-739-547 | US-09-864-761-24005 | US-09-901-484A-182 | US-09-853-526-182 | US-09-901-484A-184 | US-09-901-484A-72 | US-09-853-526-184 | | US-09-934-586A-21 | US-10-004-717-49 |) US-09-867-701-6811 | US-09-796-393-1 | US-09-898-570-9 | US-09-935-390A-5 | US-10-052-586-341 | US-10-176-758-341 | US-10-174-590-341 | US-09-898-570-11 | US-09-898-570-13 | US-09-898-570-15 |
| Sequence 365, App | Sequence 1, Appli | Sequence 523, App | Sequence 1066, Ap | Sequence 2694, Ap | Sequence 7274, Ap | Sequence 547, App | Sequence 24005, A | Sequence 182, App | Sequence 182, App | | Sequence 72, Appl | Sequence 184, App | Sequence 72, Appl | Sequence 21, Appl | Sequence 49, Appl | Sequence 6811, Ap | Sequence 1, Appli | Sequence 9, Appli | Sequence 5, Appli | Sequence 341, App | Sequence 341, App | Sequence 341, App | Sequence 11, Appl | Sequence 13, Appl | Sequence 15, Appl |

; NUMBER OF SEQ ID NOS: 15112 ; SEQ ID NO 12506 ; LENGTH: 216 ; TYPE: DNA ; OTHER INFORMATION: Clone ID: 53-LIB34-065-Q1-E1-F2 US-09-960-352-12506 RESULT 1 US-09-960-352-12506 Sequence 12506, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION: APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nagappan TITLE OF INVENTION: MUSCLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION APPLICATION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511,006/37-21(10298)C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24

ALIGNMENTS

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74 GAACTCTGTGGTGTGCTCCTGCGCCC 99

CAGCGAGGTGCGGGTGCTCCTGCGCGC 143

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Query Match Best Local Similarity

54.0%; 76.7%;

Score 54; DB 10; Length 216; Pred. No. 5e-09;

Matches

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Conservative

0; Mismatches

20;

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В

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RESULT 2 US-09-960-352-5863

Sequence 5863, Application US/09960352 Patent No. US20020137139A1 GEMERAL INFORMATION:

APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing

Tao, Nengbing

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 424
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 25-LIB34-026-Q1-E1-G1
US-09-960-352-5863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-867-701-3188/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                          GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                                                                                                                                                Sequence 780, Application US/10044090 Patent No. US20020137081A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3188, Application US/09867701 Patent No. US20020132237A1
                    CURRENT APPLICATION NUMBER: US/10/044,090 CURRENT FILING DATE: 2002-01-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/867,701 CURRENT FILING DATE: 2001-05-29
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 295
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                        108 TGCAGCCAGGAGAACGGGGGCTGCCTCCAGATCTGCCACAACAAGCCGGGTAGCTTCCAC 49
                                                                                                                                                                                                                                                                                                    87 TGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                 27 TGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGAACAGAACTCTGTGGTG 86
                                                                                                                                                                                                                                                                            48 TGTTCCTGCCACAG 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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63.5%;
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Pred. No. 6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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RESULT 6
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Best Local Similarity
Matches 47; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 40
LENGTH: 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, Application US/10001189 Patent No. US20020173634A1 GENERAL INFORMATION:
                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION TITLE OF INVENTION: VECTOR PIGGYBAC FILE REFERENCE: 835910-92098

FILE REFERENCE: 835910-92098

CURRENT APPLICATION NUMBER: US/10/001,189

CURRENT FILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: 60/244,984

PRIOR PILING DATE: 2000-11-01

PRIOR PILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 60/244,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PERL Program SEQ ID NO 780 LENGTH: 7132
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 70 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FRASER JR., MALCOLM J. APPLICANT: LI, XU APPLICANT: BEAM, TERESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: ITR Cartridge OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                   298 TCCCAGGTGGCCT 286
                                                                                                                  358 CTGATGCGCTTCGGGCTGACCATCCGGAACTGTGTCCGGAAAAGCCGGCGACGAACTGGTA 299
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                                                                                                                                        18 CGGAAGCTCTGCACCTGGACAACCGGGGACTGTGACCAGGTTCTGCCACGAGGAGGAAGAAC 77
                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 GAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGAACAGAACTC 79
                                                                                       TCTGTGGTGTGCT 90
                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                               Score 28.2; DB 9;
Pred. No. 2.2;
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                                                                                                                                                                                            Gaps
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Sequence 41, Application US/10001189
Patent No. US20020173634A1
GENERAL INFORMATION:

APPLICANT: FRASER JR., MALCOLM J. APPLICANT: LI, XU

APPLICANT:

BEAM,

US-10-001-189-41/c

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; LOCATION: (344)..(922)
US-10-001-189-46
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                                                                                                                                                                                                                                                              Query Match
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SEQ ID NO 46
LENGTH: 4613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION TITLE OF INVENTION: VECTOR PIGGYBAC FILE REFERENCE: 835910-92098 CURRENT APPLICATION NUMBER: US/10/001,189 CURRENT FILING DATE: 2001-10-30 PRIOR APPLICATION NUMBER: 60/244,984 PRIOR APPLICATION NUMBER: 60/244,984 PRIOR PILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 60/244,677 PRIOR FILING DATE: 2000-11-31 NUMBER: 60/244,677 NUMBER: 
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SEQ ID NO 41
LENGTH: 3662
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APPLICANT: BEAM, TERESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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651 CTGATGCGCTTCGGGCTGACCATCCGGAACTGTGTCCGGAAAAGCCGCGACGAACTGGTA 592
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                                                18 CGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGGTTCTGCCACGAGGAACAGAAC 77
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                                                                                                                                                                                                                           Local
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                                                                                                                                                                                   45;
                                                                                                                                                         h 28.2%; Score 28.2; DB 9; Length 4613; Similarity 61.6%; Pred. No. 3.7; 45; Conservative 0; Mismatches 28; Indels 0
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pred. No. 3.5;
0; Mismatches 28;
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                                                      SOFTWARE: Pater
SEQ ID NO 54
LENGTH: 4943
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CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER: OF SEO ID NOS: 70
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Patent No. US20020173634A1
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SEQ ID NO 53
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Best Local (
                                                                                                            PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
                                                                                                                                                                                                                                                       APPLICANT: FRASER JR., MALCOLM J.
APPLICANT: LI, XU
APPLICANT: BEAM, TERESA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MENIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
FILE REFERENCE: 835910-92098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 53, Application US/10001189 Patent No. US20020173634A1 GENERAL INFORMATION:
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2001-10-30
    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION FILE REFERENCE: 835910-92098
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: pXL-Bac-ECFP OTHER INFORMATION: sequence
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                                        TYPE: DNA
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RESULT 11
US-10-001-189-56/c
US-10-001-189-56/c
; Sequence 56, Application US/10001189
; Patent NO. US20020173634A1
; GENERAL INFORMATION:
; APPLICANT: FRASER JR., MALCOLM J.
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APPLICANT: LI, XU
APPLICANT: LI, XU
APPLICANT: BEAM, TERESA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATIC
TITLE OF INVENTION: VECTOR PIGGYBAC
FILE REFERENCE: 835910-92098
; CURRENT APPLICATION NUMBER: US/10/001,189
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CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-11-03
NUMBER: 05-880, ID. NOS: 70
COLUMN OF SECULATION NUMBER: 05/2014,677
PRIOR FILING DATE: 2000-11-31
NUMBER: 05-880, ID. NOS: 70
COLUMN OF SECULATION NUMBER: 05/244,677
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mes 45; Conserv
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Pred. No. 3.8;
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Pred. No. 3.8;
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                                                                                                                                 EUKARYOTIC TRANSFORMATION
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RESULT 13
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                                                                                                                                                                                        Matches
                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 51
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Best Local Similarity
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CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
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                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                           1016 TCCCAGGTGGCCT 1004
                                                838 TCCCAGGTGGCCT 850
                                                                               78 TCTGTGGTGTGCT 90
                                                                                                                                                                                          Local Similarity nes 45; Conserv
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                                                                                                                                                                                      Conservative
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Pred. No. 3.8;
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US-10-001-189-52

; Sequence 52,

Application US/10001189

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OTHER INFORMATION: sequence
US-10-001-189-48
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OTHER INFORMATION: Description of Artificial Sequence: pXL-Bac-EGFP OTHER INFORMATION: sequence
US-10-001-189-52
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; LENGTH: 8999
; TYPE: DNA
                                                                                                                    Query Match
Best Local Similarity
                                                                                    Matches
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PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
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SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: BEAM, TERESA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING
TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION
TITLE OF INVENTION: VECTOR PIGGYBAC
FILE REFERENCE: 835910-52098
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
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TYPE: DNA
ORGANISM: Artificial Sequence
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18 CGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGAACAGAAC 77
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Local Similarity 61.6%;
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                                                                                    Conservative
                                                                                                                28.2%; Score 28.2; DB 9; 61.6%; Pred. No. 4.4;
                                                                            0; Mismatches
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    Job time
Search completed: January 15, 2003, 22:32:21 Job time: 36.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20020173634A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                Matches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/001,189
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,984
PRIOR FILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,677
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSPOSITION USING TITLE OF INVENTION: MINIMAL SEGMENTS OF THE EUKARYOTIC TRANSFORMATION FILE REFERENCE: 835910-92098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRASER JR., MALCOLM J. APPLICANT: LI, XU APPLICANT: BEAM, TERESA
                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: p(PZ)-Bac-ECFP OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 9012
                                                                                   8666 TICCCAGGTIGGCCT 8678
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compus
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B1757668 603028107 ·
AL553470 AL553470
BQ882177 AGENCOURT
AL521984 AL521984
AL570383 AL570383
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| 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | 0.8 | | 0.8 | 0.8 | 0.8 | 1.4 | 1.4 | 1.4 | 1.4 | 1.6 | | ν | w | ω | w | 5.6 | 2 | 6.4 | 7.6 | 39 | 39 | 9 | 3.6 | 2.8 | 5.4 | 5.4 | 5.4 | 5.4 | 5.4 | ٥. | 6.8 | | 8.4 | 8.4 | |
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| 13 | 13 | 13 | ω ω | ü | 14 | 14 | 12 | ø | 12 | 12 | 10 | 10 | 10 | ø | Φ | 17 | φ | 0 | | ω | w | 0 | 7 | ω | 12 | N | ω | N | N | 2 | 2 | ū | 3 | Ψ | 2 | 14 | 4 | ω u | |
| 175259 | 183341 | 05054 | I54773 | 155243 | 33092 | LJI | 71084 | 29329 | 91273 | G12215 | 8065 | 80426 | B79874 | 85204 | 14493 | 502 | 858 | 96 | 60 | 38 | 27 | 3 | 8 | 8 | BG641885 | 41 | 6 | 35 | 85 | F532 | 384 | 1257 | 328 | 25560 | 8389 | 2133 | 92629 | M546 | |
| 1752594 60302843 | 833415 60308806 | 050541 60363282 | 547738 603: | 552439 60319613 | 0929 MRO-ET01 | 95121 | 710842 pgl: | 93295 zt28c | 12734 PM1-UT01 | 122154 602: | 806529 BB80 | 804261 BB8 | 98742 BB79 | 852041 UI-M | 49301 mt04e(| 210754 Tetra | 869 AV2858 | 796863 вв796 | 176034 mt04e(| 38559 IpLvi | M427276 pgf2r | W133828 fil2d | L233851 Tetra | I468182 ESTO | BG641885 pgllc.pk0 | G641612 pgllc | 1146007 60291 | F235332 60202 | F385197 60204 | 32104 60207 | F384882 60204 | 257017 60297 | 1328381 60298 | 255604 u156a(| E838990 RC6-E | 1335 zb55f03 | M926296 AGENCOU | M546790 AGE | |

ALIGNMENTS

RESULT 1 BE839155/c LOCUS SOURCE ORGANISM COMMENT REFERENCE KEYWORDS VERSION DEFINITION JOURNAL MEDLINE TITLE AUTHORS 407 bp mRNA linear EST 22-SEP-2000 RC6-FN0138-110800-012-E07 FN0138 Homo sapiens cDNA, mRNA sequence. BE839155 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Res.
Rua Prof. Antonio Prudente 109, Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 407) Tel: +55-11-2704922 Fax: +55-11-2707001 Brazil Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) sequence tags Shotgun sequencing of the human transcriptome with ORF expressed Simpson, A.J. Homo sapiens BE839155.1 GI:10271442 Research 4 andar, 01509-010, Sao Paulo-SP,

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FEATURES
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TITLE
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                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov m column: 01

Plate: LLAMM1497 row: m column: 01

High quality sequence stop: 716.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 716) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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BI757668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI757668 716 bp mRNA linear EST 25-SEP-2001 603028107F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5198760 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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High quality sequence start: 18
High quality sequence stop: 352.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-RC6-FN0138-110
800-012-E07st3-2000-08-11&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-Torgan: prostate_normal: Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                /clone="IMAGE:5198760"
/clone_lib="NIH_MGC_114"
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                            /lab_host-"DH10B"
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/clone_lib="FN0138"
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98.9%;
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11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 844)
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                                                                                                                                                                            http://fulllength.invitrogen.com<sup>a</sup>
231 c 244 g 137 t 1
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/clone_lib="LTL_NFL006_PL2"
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/note="Vector: pCMVSPOR
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                                                       AL521984 LTI_NFL004_NBC2 Homo sapiens cDNA clone CSODB007YC01
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AL521984.1 GI:12785477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ычый 2177 882 bp mrNA linear EST 16-AUG-AGENCOURT_7978442 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6185224 5', mrNA sequence.
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1 (bases 1 to 882)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Library technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pCMV-SPORT6 (Life Technologies); Site_1: Not1; Site_1: Sal1; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6185224"
/clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
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/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope
                                                                                               BP 191
Email:
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1 (bases 1 to 984)
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segrefégenoscope.cns.fr. Web : www.genoscope.cns.fr.
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                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone-"CSODIO20YH13"
                                                                         Location/Qualifiers
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/lab_host="DH10B"
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/sex-"male"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technolcjies, Inc.
CDNA Library Preparation: Life Technolcjies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imaqe.llnl.gov
plate: LLAM12711 row: e column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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BM546790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
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/note-*Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036.*
                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:5723510"
/clone-"INIH_MGC_125"
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/tissue_type="placenta"

/note="vector: pCNVSPORT 6; Site_1: NotI; 1st strand cDNA

was primed with a NotI oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

vefter Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@lifetech.com URL:
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                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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Pred. No. 7.5e-16;
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452 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 481
                                                                            392 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 451
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                                       71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                    11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
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                                                                                                                                                                        89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2818 row: i column: 19
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National Institutes of Health, Mammalian Gene Collection (MGC)
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[] (bases 1 to 1211)
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                                                                                                                                                                                                                                                                /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NTH_MGC Library."
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/db_xref="taxon:9606"
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  156
                   71 ACAGAACTCTGTGGTGTGCTCCTGCGCCC 99
                                                                                 96
                                                                                                                     11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                               ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 155
ACAGAACTCTGTGGTGTGCTCCTGCGCCC 184
                                                                                                                                                                88;
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w21335
w21335
zb55f03.rl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
IMAGE:307517 5' similar to gb:m57285 COAGULATION FACTOR X PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Theory Length, 1028 Std Error, 0 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 424.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044478
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                                                                                                                                                                                    Similarity
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314 286 1810
                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1250929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:307517"
                                                                                                                                                                               87.48;
98.98;
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                                                                                                                                                                               Score 87.4; DB Pred. No. 1e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132
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                                                                                                                                                                                                              ui56a05.yl Sugano mouse liver mlla Mus musculus cDNA clone IMAGE:1886384 5' similar to gb:M57285 COAGULATION FACTOR \chi
                                                                                                                                                                                                                                                                                                                                                           AI255604
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High quality sequence stop: 307.
Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-RC6-FN0138-260
700-011-G08&t3-2000-07-26&t4-1)
Seq.primer: puc 18 forward
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EST:
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                                                                                                                                                          PRICURSOR (HUMAN);, mRNA sequence.
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Ludwig Institute for Cancer Research
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 472)
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/clone_lib="FN0138"
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Pred. No. 1.6e-15;
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                                                                                                                                       BI328381 596 bp mRNA linear EST 30-JUL-2001 602985811F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5138306 5',
                                                                                              BI32838]
                                                                                                                     mRNA sequence.
Mus musculus
                                                                     BI328381.1 GI:15013038
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL"
/db_xref="taxon:10090"
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Pred. No. 3.7e-09;
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                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM11302 row: a column: 16
                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 758)
High quality sequence start: 3 High quality sequence stop: 756
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758 bp mRNA linear EST 20-JUL-2001
602978857F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5123607 5',
                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BI257017
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11340 row: f column: 03
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/clone_lib="NCI_CCAP_Li9"
/clone_lib="NCI_CCAP_Li9"
/lab_bost="NH108 (Tl phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Sycrage insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
Plate: LLAM9531 row: b column: 21
High quality sequence stop: 690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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  Conservative
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
04 a 184 c 231 g 152 t
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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a 171 c 223 g 164 t
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                    65.4%;
86.7%;
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                  Score 65.4; DB 12
Pred. No. 4.4e-09;
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Pred. No. 4
    Mismatches
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                                      DB 12;
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  Indels
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TITLE
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                                      TCTGTGGTGTGCTCCTGCGCCCG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov f column: 08
High quality sequence stop: 722.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                         Conservative
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 %b. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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86.7%;
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Search completed: January 15, Job time: 1273 secs

2003, 21:18:47

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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| Altsi Lipsi WPI; | (WHED | 31-MAR- | 30-MAR | 05-0 | W020005 | Homo | Single diseas neurol | Single | 09-FEB- | AAC70860 | RESULT 1 AAC70860 ID AAC70860 XX | | 44 | 43 | 41 | 40 | ω (Θ (| 36 37 | ω L | ω W | 32 2 | 30 | 2 20 | 26 27 | 25 | 23 | 220 | 19 | 17 | 15 5 | 14 | 12 | 10 11 |
| huler D hutz RJ 2000-6 | ال ا | 1999 | AR-2000; | -OCT-2000 | 8519 | sapiens | e nucl se sus logica | le nucleo | EB-2001 | 0860; | st | | 28.6 28.6 | | N | 29 29 | 29 | | | | | | | | | | 30.8 | | | | | | |
| D, Cargi W, Patil | WHITEHEAD : | ; 99us- | | • | -A2. | .s | eotide po ceptibili l system; | tide | (firs | | andard; | | 28.6 28.6 | | | | | | | | | | | | | | | | | | | | 88.4 |
| 11 M, | INST BI | 01272 | 2000WO-US08440 | | | | lymc ty; for | polymorphism | t entry | | DNA; 3 | | 719 1875 | 405 | 2565 | 2013 2565 | 2013 | 6813 | 4901 | 3810 | 2909 3747 | 2196 | 2196 | 4801 1743 | 7037 4181 | 2461 4790 | 17902 295 | 13923 | 1860 | 300 | 1507 1887 | 1467 | 1467 |
| Dale klar | OMED | 48. | 40. | | | | phis ardi | phis | ٢ | | 167 в | | 23 23 | wĸ | , ,,- | ω | N 0 | υw | ωu | ω, | ωω | ωω | ω (| ωN | 00 | 27 | æω | ωυ | N | SN | N H | N | 9 |
| ey GQ, Ireland JS, P; | IOMEDICAL RES. | | | | | | SNP; human; geneti scular system; end sting; paternity t | m containing sequence | | | , af | ALIGNMENTS | ABL05065 AAS85741 | ABL96473 | ABL92086 | ABL97387 ABL92075 | AAL03051 | AAS85740 | AAS92853 | AAS82533 | AAS73293 AAS73044 | AAS85733 AAS89351 | AAS82534 | AAD06781 AAS85732 | AAS45066 AAD06778 | AAT41544 AAS45254 | ABL80210 | ABL05109 | AAF24738 | AAH57261 | AAA54031 AAH57469 | AAF59409 | AAV56776 |
| Lander ES; | | | | | | | c disease; locrine system; esting; ds. | #230. | | | | | סים | Human reproductive | n Tumour | testicula | encoding nove an reproductiv | encoding nove | DNA encoding novel | DNA encoding novel | DNA encoding novel | DNA encoding novel | DNA encoding novel | Human haematopoiet | cDNA encoding nove | Human gas6-encodin | Drosophila melanog Human ovarian canc | Serine protease fo Drosophila melanog | Nucleotide sequenc | Human liver specif | fact | Human Factor X gen | Factor |

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RESULT 2
AAC70878
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                                             Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing,
Claim 1; Fig 5; 214pp; English
                                    medicine and genetic analysis -
                                                                                                                                                       Altshuler D,
Lipshutz RJ,
                                                                                                                       WPI; 2000-611722/58.
                                                                                                                                                                                                                                                                                              30-MAR-2000; 2000WO-US08440
                                                                                                                                                                                                                                                                                                                               05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                 WO200058519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine sys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single nucleotide polymorphism containing sequence #236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC70878 standard; DNA; 367
                                                                                                                                                                                                          (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                        (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC70878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where th nucleotide may be C or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, aliele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 367 BP; 66 A; 122 C; 103 G; 75 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 GCCACGAGGAACAGAACTCTGTGGTGCTGCTGCGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                       Cargill M,
Patil N,
                                                                                                                                                                                                                                                            99US-0127248
                                                                                                                                                                                                                                                                                                                                                                                                                             lity; cardiovascular system; endocrine system;
n; forensic testing; paternity testing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                         Sklar
                                                                                                                                                                       Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100; B 21; Length 367; Pred. No. 3.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                       Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                     Lander ES;
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RESULT 3
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The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be
                                                                                                                                              Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing,
                                                                                                          Claim 1; Fig
                                                                                                                                     medicine and genetic analysis -
                                                                                                                                                                                                                        WPI; 2000-611722/58.
                                                                                                                                                                                                                                                       Altshuler D,
Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                         31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000; 2000WO-US08440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single nucleotide polymorphism containing sequence #238
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200058519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-FEB-2001
                                                                                                                                                                                                                                                                                                     (WHED ) WHITEHEAD INST BIOMEDICAL RES. (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC70884 standard; DNA; 367 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where th nucleotide may be C or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 367 BP; 67 A; 121 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCCACGAGGAACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                        5; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                       Patil N,
                                                                                                                                                                                                                                                                      Cargill M,
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                                                                                                                                                                                                                                                        Sklar P;
                                                                                                                                                                                                                                                                   Daley GQ, Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99.6;
Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents a polymorphism where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311
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                                                                                                                                                                                                                                                                     Lander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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PT PD XXX
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                                   WPI; 1991-224839/31.
P-PSDB; AAR13675.
New factor X-LACI hybrid protein - comprises light chain of factor X and LACI's first kunitz domain for use as anticoagulant
                                                                                                                     25-JAN-1990;
                                                                                                                                                                                         EP439442-A.
                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                       Girard TJ,
                                                                                              (UNIW ) UNIV OF WASHINGTON
                                                                                                                                             21-JAN-1991;
                                                                                                                                                                    31-JUL-1991.
                                                                                                                                                                                                                                       misc_RNA
                                                                                                                                                                                                                                                                        misc_RNA
                                                                                                                                                                                                                                                                                                                                              misc_RNA
                                                                                                                                                                                                                                                                                                                                                                               misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Factor X-LACI hybrid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ12776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ12776 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 367 BP; 66 A; 122 C; 103 G; 75 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where th nucleotide may be C or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                schizophrenia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACGAGGAACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCTTTGGCAGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGGACTGTGACCWGTTCT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                       Broze GJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                     90US-0470289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological systems, such as coronary artery disease, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                           91EP-0870008
                                                                                                                                                                                                                                                                                                                                                                                                                                                 blood; coagulation; inhibitor; Factor x;
TF; Lipoprotein-Associated Coagulation Inhibitor;
                                                                                                                                                                                                                                    /label GLA_domain
285..471
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 22..771
                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                              535..771
                                                                                                                                                                                                                                                                                                                                                                              /label- X-LACI
22..534
                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                        label= xlc
                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                     'label- kunitz_domain
                                                                                                                                                                                                                                                                                                                                 '*tag=
                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.6%;
99.0%;
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                                                                                                                                                                                                              growth_factor_domains
                                                                                                                                                                                                                                                                                   pre-pro_leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           788 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367;
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AAX15427
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AVM; meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis; dermatitis; endometriosis; angiofibroma; rheumatoid arthritis; atheroscelotic plaque; corneal graft neovascularisation; haemophilic joint; hypertrophic scar; Osler-Weber syndrome; pyogenic granuloma retrolental fibroplasia; scleroderma; trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Truncated tissue factor; tissue factor binding ligand; coagulation; disease-associated vasculature; tumour; benign prostatic hyperplasia; diabetic-retinopathy; vascular restenosis; arteriovenous malformation;
                      Example 9; Columns 129-132; 83pp; English.
                                                                Tissue factor binding ligands - comprising first binding region which binds to vasculature, particularly of tumours, and tissue
                                                                                                                 WPI; 1999-189722/16
                                                                                                                                               Edgington TS,
                                                                                                                                                                      (SCRI ) SCRIPPS RES INST. (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                           05-MAR-1992;
02-MAR-1994;
                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding coagulation factor X/Xa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The protein is used as a blood coagulation inhibitor in mammals. It is believed to mimic the Xa/LACI complex in binding to and inhibiting VIIa/tissue factor. LACI inhibits via a novel feedback mechanism requiring generation of Xa (a prod. of VIIa/TF activity); XICLACIki inhibits VIIa/TF activity directly.

The DNA allows prodn. of XICLACIki by introduction of the gene into cells suitable for expression, e.g. E. coli or CHO cells.
                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                    02-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 788 BP; 230 A; 187 C; 209 G; 162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        vascular adhesion; coagulation factor; factor X/Xa; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12-14; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                        95US-0479733.
92US-0846349.
94US-0205330.
94US-0273567.
                                                                                                                                               Thorpe PE
                                                                                                                                                                                                                                                                                                      95US-0479733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88.4; DB 12; Pred. No. 1.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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The present sequence encodes a coagulation factor.

The specification

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سم.
       RESULT 6
AAA89786
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Best Local s
The present invention relates to a binding ligand with a first binding region that is operatively linked to either a coagulation factor or a second binding region that binds to a coagulation factor. The first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue factor protein; truncated tissue factor; tTF; cytostatic; coagulant; diabetic retinopathy; arteriovenous malformation; meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis; endometriosis; hemophylic joint; hypertrophic scar; vascular adhesion; tumour; cancer; ligand; human; factor X; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    describes tissue factor binding ligands which comprise a binding region which binds to vasculature, particularly of tumours, and a tissue factor construct. The binding ligands can be used for stimulating coagulation in disease associated vasculature, particularly for the treatment of tumours. The products can also be used for treating e.g. benign prostatic hyperplasia, diabetic retinopathy, vascular restenosis, arteriovenous malformations (AWM), meningioma, hemangioma, neovascular glaucoma, psoriasis, synovitis, dermatitis, endometriosis, angiofibroma, rheumatoid arthritis, atheroscelotic plaques, corneal graft neovascularisation, haemophilic joints, hypertrophic scars, Oster-Weber syndrome, pyogenic granuloma retrolental fibroplasia, scleroderma, trachoma, or vascular adhesions. The products can also be used in binding assays.
                                                                                                                       New immunological and growth factor-based bispecific binding ligands, useful for stimulating coagulation in vasculature-associated diseases, useful for treating both benign and malignant diseases (e.g. meningioma
                                                                        Example 9; Column 129-130; 83pp; English.
                                                                                                              or hemangioma)
                                                                                                                                                                                                                                                                                                                                             05-MAR-1992;
02-MAR-1994;
                                                                                                                                                                                                    WPI; 2000-531471/48.
                                                                                                                                                                                                                                      Edgington TS,
                                                                                                                                                                                                                                                                      (SCRI ) SCRIPPS RES INST. (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6093399-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding coagulation factor X/Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA89786 standard; DNA; 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                  Thorpe PE;
                                                                                                                                                                                                                                                                                                                          92US-0846349.
94US-0205330.
94US-0273567.
                                                                                                                                                                                                                                                                                                                                                                                                 9505-0482369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.48;
98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88.4; DB 20;
Pred. No. 1.9e-18;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1126;
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CCC PS PT PT XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC binding region binds to a component on the surface of a tumour. The CC second binding region is all or part of an antibody. An example of a CC coagulation factor for use in the invention is human truncated tissue CC factor. Truncated tissue factor (tTF) is the extracellular domain of the CC invention is useful for stimulating coagulation in vasculature CC associated diseases. Particularly, the binding ligand of the CC component. These diseases include benign growths (e.g. BPH), diabetic CC component. These diseases include benign growths (e.g. BPH), diabetic CC retinopathy, arteriovenous malformations, meningioma, hemongloma, CC neovascular glaucoma, psoriasis, synovitis, endometriosis, hemophylic CC ligands offer the advantage that even limited damage to the tumour CC vasculature could produce an avalanche of tumour cell death because CC each capillary provides oxygen and nutrients for thousands of tumour CC cells. The present sequence is DNA encoding coagulation factor vas used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                     05-MAR-1992;
02-MAR-1994;
11-JUL-1994;
                                                                                                                WPI; 2000-269871/23.
                                                                                                                                            Edgington TS, Thorpe PE;
                                                                                                                                                                          (TEXA ) UNIV TEXAS SYSTEM (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                14-MAR-2000
                                                                                                                                                                                                                                                                                                                                             US6036955-A.
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                       vascularised
                                                                                                                                                                                                                                                                                                                                                                                                               tumour vasculature; bispecific antibody; targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                             Truncated tissue factor; tTF; human; blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding Factor X/Xa, SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA12970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA12970 standard; DNA; 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                     92US-0846349.
94US-0205330.
94US-0273567.
                                                                                                                                                                                                                                                                               95US-0479727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 88.4; DB 21; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1126;
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                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the
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The invention relates to the induction of blood coagulation specifically

Example 9; Columns 131-132; 86pp; English.

Kit for inducing coagulation in tumor vasculature, useful for treating malignant or benign growths, contains ligand, linked to coagulation agent, that targets tumor marker -

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A.X. ACC DE A.X. A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC tumour vasculature; such proteins include vascular endothelial growth CC factor (PEGF) and members of the fibroblast growth factor (PEGF) may be incorporated into the bispecific molecule in order to target coagulation to tumour vasculature. The coagulation factor-binding portion of the bispecific molecule may be, for example, directed to target coagulation CC to tumour vasculature. The coagulation factor-binding portion of the bispecific molecule may be, for example, directed to tissue factor (TF). CC Apreferred form of TF used in the invention is a truncated form (TF). CC Although tTF can associate with Factor VIIa, the tTF/Factor VIIa complex CC cannot alone initiate the coagulation cascade as the complex has to be associated with a phospholipid surface for coagulation to occur. CC However, binding of tTF to tumour vasculature via a tumour antigen/tTF bispecific antibody brings tTF into close enough proximity with the cell membrane to enable the initiation of coagulation. Kits for the induction of tumour vasculature-specific coagulation may be used to treat malignant corporate to enable the initiation of coagulation is restenosis, psoriasis, glaucoma, rheumatoid arthritis. Coagulation is induced care likely to be effective against many different types of cancer. Such kits represent PCR primers used in exemplifications of the present invention for constructs encoding tTF. TTF variants or tTF dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ56120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
   05-MAR-1992;
02-MAR-1994;
11-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                within tumour vasculature. This is achieved by the use of a bispecific molecule, which comprises a region capable of binding to intratumoral vascular or stromal cells linked to a coagulation factor or to a region capable of binding to a coagulation factor. An example of such a bispecific molecule is a bispecific antibody, where one arm binds a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vitamin-K dependent coagulation factor; tumour associated vaso carcinoma; benign prostatic hyperplasia; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour antigen, and the other arm binds a coagulation factor. The expression of certain proteins (tumour antigens) is upregulated in
                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                 US6004555-A
                                                                                                                                                                                                                                                                                                                                                  Unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                       neovascular glaucoma; psoriasis; cytostatic; antidiabetic; vasotropic; ophthalmological; antipsoriatic; Factor X/Xa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular restenosis; arteriovenous malformation; meningoma; haemangioma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitamin-K-dependent coagulation factor X/Xa coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ56120 standard; DNA; 1126 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1126 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                generate constructs encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
92US-0846349.
94US-0205330.
94US-0273567.
                                                                                                                                        95US-0487427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 A; 341 C; 342 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tTF, tTF variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour associated vasculature;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or tTF dimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Human

Factor X protease cDNA.

Factor X; factor IX; serine protease activity; catalytic domain; zymogen-activating domain; epidermal growth factor-like domain; EGF2; regulator; coagulation; fibrinolysis; homeostasis; X-ray si

detection; drug modelling; restriction protease;

RESULT 9 AAV10462

AAV10462;

16-JUN-1998

(first entry)

AAV10462 standard; DNA;

1404 BP

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8

11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70

ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA

Best Matches

Local

Similarity

88.4%; 98.9%;

; 68

Conservative

0; Score Pred.

Mismatches

88.4; No. 1

.9e-18; DB 21;

Length 1126;

0,

Gaps

Sequence 1126

BP; 269 A; 341 C;

342 G;

174 T; 0 other;

밁 Ş

87 71 27

ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100

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tumour-associated vargulature which is benign or malignant. The method C can be used to treat cancer by promoting specific blood coagulation in the vasculature of the tumour relative to the vasculature in nontumour cities. Vascularised tumours are usually solid tumours, particularly CC carcinomas which require a vascular component to provide oxygen and cultients. The ligands are suitable to treat benign and malignant CC diseases with a vascular component, including benign prostatic CC hyperplasia, diabetic retinopathy, vascular restenosis, arteriovenous califormations, meningioma, haemangioma, neovascular glaucoma and CC psoriasis. The ligands can also be used in standard binding assays in CC vitro. Bispecific ligands can be designed which are capable of binding to conscular endothelial cells and disease-associated agents such as CC vascular endothelial cells and disease-associated agents are similar in CC different dieases and in different tumours, making it possible to treat cumerous diseases and indifferent types of cancer with one pharmaceutical, therefore an agent dows not need to be tailored to each individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the coding sequence for Factor X/Xa, a vitamin-K-dependent coagulation factor. This coagulation factor can be used in the formation of coaguligands. Mutated versions of this sequence can be used in the method for delivering a coagulant to a tumour-associated vasculature using bispecific binding ligands which promote blood coagulation. The binding ligand consists of identify the promote binds to a surface-expressed, surface accessible or surface-localised component of itumour cell, intratumoural vasculature or tumour associated stroma. The binding recommendation of itumour cell, intratumoural vasculature or tumour associated stroma. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bispecific binding ligands for promoting blood coagulation in a tumour associated vasculature are useful for treating cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding region is linked to a coagulating agent which is a coagulation factor (e.g. tissue factor). The second binding region comprises an antibody or an antigen binding region of an antibody. The method is use for delivering an exogenous or an endogenous coagulation factor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Column 131-132; 83pp; English
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                                                  tumour type.
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Homo sapiens

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                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes a human factor X protease. This protein is used CC in the construction of a novel non-glycosylated protein and truncated CC and zymogen forms of this protein, which have serine protease activity. The protein is composed of various domains from a factor IX family CC protein, namely a catalytic domain (CD) N-terminally bound to a CZ zymogen-activating domain (ZAD), N-terminally bound to an EGF1 and/or CC grotein (EGF2 domain (ZAD), N-terminally bound to an EGF1 and/or CC (are used to identify activators/inhibitors of factor IX family proteins CC (potentially useful as regulators of coagulation, fibrinolysis and CC homeostasis). The protein in zymogen form is also useful in assays for CC detecting factor IX a activity in aqueous solution (specifically in body CC fulids). The protein can be used to produce co-crystals with protease CC variants or inhibitors for X-ray structural analysis and drug modelling CC and as restriction proteases in biotechnology. These truncated proteins CC have the same specificity as factor IX family proteases and can be CC produced in prokaryotes in a form that allows production of active enzyme CC by conversion to native form and enzymatic cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
Human Factor X genomic DNA
                                   27-NOV-1998
                                                                                                     AAV56776 standard;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1404 BP; 356 A; 404 C; 423 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-glycosylated, truncated forms of factor IX family protein with serine protease activity - used to screen for specific modulators
                                                                                                                                                                                        375
                                                                                                                                                                                                                                                   315 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 49pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and to assay factor IXa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hopfner K, Kopetzki E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1996;
11-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-1997.
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                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                   11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                        ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                       ACAGAACTCTGTGGTGTGCTCCTGCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-052304/05
                                                                                                                                                                                                                                                                                                                            ; 68
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                          Conservative
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96EP-0110959.
96EP-0109288.
96EP-0110109.
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/note= "partial 
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                                                                                                                                                                                                                                                                                                                                        88.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "partial coding sequence"
                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                        Score 88.4;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                        DB 19;
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                                                                                                                                                                                                                                                                                                                                                       Length 1404;
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                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 11 AAV56821

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This sequence encodes the human Factor X protein which is used in a method resulting in the production of novel human Factor X (F10) analogues. Such analogues have in the region of the natural F10a CC activation cleavage site, a modification that creates a processing site CC for a protease that does not naturally cleave F10 in this region. The CC proteins are used to generate, in vivo or in vitro, F10a analogues that CC vII or VIII, e.g.in haemophiliacs who have developed antibodies to CC factors VIII and/or IX. The encoding nucleic acid can be used in gene CC therapy of the same conditions. The analogues have high stability and can be activated without use of animal enzymes such as trypsin. Only CC The analogues can be isolated as a pure single-chain pro-protein (not usually possible because of rapid processing of the native precursor) and CC this converted to two-chain form by subsequent activation. Activated CC analogues have good stability and structural integrity and are processive information.
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                               Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             decomposition products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New factor X analogues with processing site for protease not active on natural protein - and related DNA, is very stable and can be activated in vitro or in vivo without using animal protease(s), particularly for treating disorders of blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 1; 86pp; German.
        429
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P-PSDB; AAW76216.
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                                             71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
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                                                                                                                                                11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                             Similarity
                                                                                                                                                                                                                 Conservative
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121..1464
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1..120
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                                                                                                                                                                                                                                        88.4%;
98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             b
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                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                  Score 88.4; DB Pred No. 2e-18;
                                                                                                                                                                                                                                                            DB 19; Length 1467;
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                                                                                                                                                                       CC This sequence encodes the human Factor X protein which is used in a CC method resulting in the production of novel human Factor X (F10) CC analogues. Such analogues have in the region of the natural F10a CC activation cleavage site, a modification that creates a processing site CC for a protease that does not naturally cleave F10 in this region. The CC proteins are used to generate, in vivo or in vitro, F10a analogues that CC can be used to control bleeding and for treating defects of factors IX, CC VII or VIII, e.g. in haemophiliacs who have developed antibodies to CC factor VIII and/or IX. The encoding nucleic acid can be used in gene CC therapy of the same conditions. The analogues have high stability and can CC be activated without use of animal enzymes such as trypsin. Only CC activated without use of animal enzymes such as trypsin. Only CC converted to two-chain form by subsequent activation. Activated CC usually possible because of rapid processing of the native precursor) and CC this converted to two-chain form by subsequent activation. Activated CC analogues have good stability and structural integrity and are protected to the converted of inactive intermediates and autoproteolytic
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Factor X; analogue; activation cleavage site; protease; bleeding; human; Factor IX; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 1; 82pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Factor X genomic DNA
                                                                                                                              Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New factor 10 deletion mutants lacking the natural protease processing site - but having a non-natural site inserted, and related DNA, particularly for in vitro activation to products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WP1; 1998-481212/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-1998;
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                                                                                                                                                             decomposition products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlokat U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dorner F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to treat blood coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV56821 standard; DNA; 1467
 369
               11 AGTCACAGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 428
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eibl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                              88.4%;
98.9%;
                                                               0
                                                                             Score 88.4; DB 19;
Pred. No. 2e-18;
                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmelspach M,
                                                             1;
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                                                                                              Length 1467;
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                                                                                                                              Matches
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                            The present invention describes a factor x analogue (I) which contains a modification between Glu226 and Ile235, relative to the 488 residue amino acid sequence given in AAB70411. (I) has haemostatic activity and can be used in gene therapy. (I) encoding polynucleotide (II) can be used to produce a drug, which is useful for treatment of patients with blood coagulation disorders, such as patients suffering from haemophilia, or haemophiliacs with inhibitory antibodies. Preparations containing a polypeptide with factor X/Xa activity are more readily activated by factor X1a or its derivative, which has high stability, without having to use one of the proteases used in prior art to activate the natural factor X, particularly one of animal origins, such as Russell's viper venom (RVV) or trypsin. The present sequence encodes human factor X, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel factor X analog useful for producing drug which is useful for treatment of blood coagulation disorders, such as hemophilia, conta modification between amino acids Glu226 and Ile235
                                                                                                                                                                                       Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB70411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human factor X nucleotide sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429
 429
                                                          369 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                        11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-191516/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation disorder; haemophiliac;
                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99AT-0001377
                                                                                                                                         98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                         0;
                                                                                                                                       Pred. No. 2e-18;
                                                                                                                                                        Score 88.4;
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458
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456
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                                                                                                                                                        DB 22;
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                                                                                                                         Indels
                                                                                                                                                      Length 1467;
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                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                               oligosaccharides to the activation peptide; removal of an internal tripeptide to yield two-chain factor X and removal of the propeptide just prior to secretion. While some of these modifications do not appear essential for factor X function the removal of the signal sequence, propeptide, internal tripeptide and full gamma-carboxylation are all steps which are important requisites for the production of biologically active factor X/FXa. Isolated chimeric polynucleotides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin K-dependent protein (VKDP). The fusion proteins encoded are vitamin K-dependent protein (VKDP).
                                                                                                                                                                               gamma-carboxylation enhancers and are useful for optimising the gamma-carboxylation of a VKDP to produce a fully gamma-carboxylated VKDP. The fusion proteins and recombinant cells expressing them are useful for alleviating a VKDP associated disease. The fusion constructs result in the production of fully gamma-carboxylated mature VKDPs which are biologically active. The i. rention encompasses all combinations of propeptide sequences (modified or not) and VKDP's. This sequence encodes the signal, propeptide and mature protein sequence of human Factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Efficient processing and release of mature two-chain factor X into the circulation requires: removal of the signal sequence; formation of disulfide bonds; modification of amino terminal glutamic acid residues, to gamma-carboxyglutamic acid; modification of one aspartic acid in the first epidermal growth factor (EGF) domain to Beta-hydroxyaspartic acid; addition of N- and O-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric DNA for optimizing gamma carboxylation of vitamin \kappa-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein; fusion protein; coagulation factor; Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-638152/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001
                                                                                                                                                    Sequence 1507 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 6a; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200054787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haemophilia; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
369
                                   11
ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTG GGACCAGTTCTGCCACGAGGA 428
                   AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Camire RM,
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US06934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0124609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coding sequence
                                                                                                                                                  394 A; 429 C; 446 G; 238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds.
                                                                                           88.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larson PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    removal of the signal sequence; formation
                                                                          0
                                                                                                               Score
                                                                                           Pred.
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stafford
                                                                                             No. 2e-18;
                                                                                                               88.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                        Query Match
Best Local :
                                                                                                         Matches
                                                                                                                                                                                                                  mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of [1] in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer investigation.
                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
metabolic disease; developmental disease; cytostatic; immunomodulatory;
neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (1). (1) can have cytostatic, immunomobilatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 233; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sornasse !,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-2000; 2000WO-US30396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tissue specific; diagnosis; brain; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human liver cell specific cDNA sequence SEQ ID NO:309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001
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                                     424
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                                                                 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-291057/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGAACTCTGTGGTGTGCTCCTGCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGAACTCTGTGGTGTGCTCCTGCGCCCCG
   ACAGAACTCTGTGGTGTGCTCCTGCGCCCG
                                   ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       liver; uterus; ovary; stomach;
                                                                                                         , 68
                                                                                                                        Similarity
                                                                                                                                                                                                       immunopathology or neuropathology.
                                                                                                                                                                         1887
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                         B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0163508
                                                                                                                                                                       467 A; 549 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                      88.4%;
98.9%;
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                                                                                                      0;
                                                                                                                      Score 88.4;
Pred. No. 2
                                                                                                                                                                       544 G;
                                                                                                    Mismatches
 100
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                                                                                                                                                                     327 т;
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                                                                                                                                       DВ
                                                                                                                                                                       0 other;
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                                                                                                                                       1887;
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ACAGAACTCTGTGGTGTGCTCCTGCGCCCG

513

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide CC sequences (I). (I) can have cytostatic, immunomodulatory and CC neuroprotective activities, and can be used in gene therapy. (I) and CC proteins (II) encoded by then are used in high throughput screening CC assays to select DNA molecules, RNA molecules, peptide nucleic acids, CC mimetics, peptides, proteins, agonists, antigonists, antibodies or CC their fragments, immunoglobulins, inhibitors, drug compounds and CC pharmaceutical agents. Expression of (I) in a sample indicates the CC differentiation of embryonic stem cells into a tissue selected from CC brain, heart, kidney, liver, lung, skeletal muscle or pancreatic CC disease or disorder. The gene profile can be used for diagnosis, CC prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a carrowarhology of the compounds and concern the concern
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gane is associated with a cancer, immunopathology or neuropathology -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 300 BP; 73 A; 81 C; 88 G; 44 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 107; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sornasse T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human liver specific cDNA sequence SEQ ID NO:101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001
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                                                                                                                                                           76 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 105
                                                                                71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-291057/30.
                                                                                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 85.4%; Score 85.4; DB 22; 95.6%; Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 300;
                                                                                                                                                                                                                                                                                                                                    0;
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Search completed: January 15, Job time : 154 secs

2003, 19:50:15

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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1: gb_ba:*
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2181.620 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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gb_pat:*
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gb_pl:*
em_htgo_hum:*
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                                         em_htg_mus:*
em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
em_htg_vrt:*
em_sy:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| No. Score Match Length DB 100 100.0 156 9 2 93.8 93.8 12938 9 3 93.8 93.8 132933 9 4 92 92.0 350 9 8 84.4 88.4 1126 6 6 88.4 88.4 1144 9 11 88.4 88.4 11467 6 13 88.4 88.4 1500 6 14 88.4 88.4 1500 6 14 88.4 88.4 1500 6 15 88.4 88.4 1500 6 16 72.2 72.2 49581 2 17 69.4 69.4 20130 10 21 65.4 65.4 1497 10 22 65.4 65.4 1497 10 23 65.4 65.4 1497 10 24 52.4 52.4 1554 6 25 52.4 52.4 1554 6 26 52.4 52.4 1554 6 27 45.4 45.4 1599 4 29 32.4 30.8 31.8 132171 3 31.8 31.8 31.8 15755 9 32 31.8 31.8 15755 9 33 31.8 31.8 15755 9 33 31.8 31.8 15755 9 33 31.8 31.8 15755 9 34 30.8 30.8 159743 2 39 30.2 30.2 148198 2 30 30.2 218138 2 31 30.3 30.9 56846 9 32.6 52.6 52.6 52.6 52.6 52.6 52.6 52.6 5 | AL451007 | | 9.6 11 | 29.6 | 4-4 |
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ALIGNMENTS

| REFERENCE | ORGANISM | SEGMENT SOURCE | VERSION KEYWORDS | LOCUS DEFINITION ACCESSION | RESULT 1 HUMFX5 |
|--|---|--|---|--|--------------------|
| Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 156) | DNA. Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | 5 of 8 femore sapiens (tissue library: of Lawn et al., and Yoshitake et al.) | 100394.1 GI:182826 Stuart factor; blood coagulation factor; factor X; glycoprotein; serine norterage. | HUMEYS 156 bp DNA linear PRI 09-NOV-1994 Human factor X (blood coagulation factor) gene, exon 5. | |

pred. No. is the number of results predicted by chance to have a

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TO cite this work please use: SeattleSNPs. NHLBT HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 29488)
Rieder, M.J., Armel, T.Z., Carrington, D.P., Chung, M.-W., Lee, K.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arousbil 29488 bp DNA linear PRI 22-Homo sapiens coagulation factor X (F10) gene, complete cds. AF503510
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                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                  Ocation/Qualifiers
                                                                                                                                                       frequency="0.01"
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/db_xref="taxon:9606"
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RMNVAPACLDERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKL
SSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYG
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/protein_id-"AAM19347.1"
/db_xref-"GI:20336663"
/gene="F10"
                                               /replace="g"
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join(1672. .1741,8769. .8429,17274.
19736. .1986/,22668. .22912,26198. .
                                                                      /gene="F10"
/frequency="0.22"
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/replace="t"
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/gene="F10"
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/replace="t"
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/gene="F10"
               'gene="F10"
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replace="c"
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3977
                                                                 'gene--F10
                                                                                       replace-"a"
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/replace="a"
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/replace="c"
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2757
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/replace="g"
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/replace="a"
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VERSION
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AL137002
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                                        requests: clonerequest@sanger.ac.uk Clone
on May 8, 2001 this sequence version replaced gi:13274222.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >-
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
database can be found at
http://www.senter.ac.uk/Products/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/files/fil
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al Similarity 97.9%;
95; Conservative
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA sequence from clone RP11-98F14 on chromosome 13q22.1-31.1, complete sequence.
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/frequency="0.99"
/replace=""
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/rpt_ mily="ERV1"
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/frequency-"0.01"
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7396. .7727
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Pred. No. 7.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-98F14 It may be shorter because we sequence overlapping sections only once, except for a 100 hase overlap.

The true left end of clone RP11-98F14 15 at 1 in this sequence. The true left end of clone RP11-39H12 is at 132334 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPII-98F14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The true right end of clone RP11-265C7 is at 123923 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //www.chori.org/bacpac/home.htm
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6411
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8860. .8943
Note="3 copies 20 --
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/note="3 copies 51 mer 93% conserved"
5565. .6669
'note="3 comies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
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note="4 copies 17 mer 95% conserved"

8984. .9037

/note="3 copies 18 mer 90% conserved"

9427. .9530
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/note="38 copies 16 mer 78% conserved"
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                                                                           /note="7 copies 57 mer 87% conserved"
L1050. .11091
                                                                                                                                                                                                                                               3927. .9056
/note="5 copies 26 mer 69% conserved"
                                                       'note="2 copies 21 mer 100% conserved"
                                                                                                                                 'note="4 copies 26 mer 92% conserved"
                   note="LIMC1 repeat: matches 5862. .6231 of consensus"
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າte="າດ
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                                                                                                                                                                                                                                                                     0. .9059
te="4 copies 35 mer 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                   te="4 copies 18 mer 81% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                     te="2 copies 38 mer 98% conserved"
2. .6773
te="2 copies 51 mer 93% conserved"
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                                                                                                                 .10602
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15491. .15973
/note-"CpG island"
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13806. .14155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27585. .27688 // /note="4 copies 26 mer 74% conserved" 27733. .27981
                                                                                                                                 /note="Single clone region. Sequence from reads from a
short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
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19411. .19587
/note="3 copies 59 mer 79% conserved"
                                                                                                                                                                                                                                                       31152. .3142:
                                                                                                                                                                                                                                                                                                                                                                                                               /note="Sequence from uni-directional dGTP big dye
terminator reads only."
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/note="15 copies 35 mer 61% conserved"

30911. .31412 -- 7 mar rd 61% conserv
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                                                                        31268
                                                                                                                                                                                                                                                                                                                   /note="7 copies 53 mer 63% conserved" 31078. .31415 copies 26 mer 62% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="14 copies 32 mer 61% conserved"
30987. .31385
/note="7 copies 57 mer 64% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="17 copies 28 mer 61% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="251 copies 2 mer gg 61% conserved"
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/note="Tandem repeat. Forced join. Gap size estimated to
                                                /note="9 copies 16 mer 64% conserved"
                                                                                    /note="12 copies 21 mer 61% conserved"
                                                                                                                                                                                                                               /note="9 copies 30 mer 61% conserved"
                                                                                                                                                                                                                                                                             /note=*6 copies 47 mer 66% conserved*
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                                                                                                                                                                                                                                                                 Submitted (22-JUL-1997) Tomohiro Hayashi, Yamagata University School of Medicine; 2-2-2 Iida-Nishi, Yamagata, Yamagata 990-; Japan (E-mail:thayashi@med.id.yamagata-u.ac.jp, Tel:+81-236-28-5316, Fax:+81-236-28-5318)

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                              Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens mononuclear cell DNA. Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coagulation factor X; F10.
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71~72
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Pred. No. 7.2e-18;
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                                                         Sequence 27 from patent US 6093399 ARI03990
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Thorpe, P.E. and Edgington, T.S.
Methods for the specific coagulation of vasculature
Patent: US 6004555-A 27 21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 27 from patent US 6004555. R095306
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/codon_start=1
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1 (bases 1 to 1126)

Leytus, S.P., Chung, D.W., Kisiel, W., Kurachi, K. and Davie, E.W. Characterization of a cDNA coding for human factor x

Proc. Natl. Acad. Sci. U.S.A. 81 (12, 3699-3702 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         In processing, factor X (Stuart factor) is converted to Xa by cleavage of a glycopeptide from the amino-terminal end of the heavy chain. It then acts as a serine protease in converting prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human liver, cDNA to mRNA, clone Homo sapiens
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Thorpe, P.E. and Edgington, T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent: US 6093399-A 27 25-JUL-2000;
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                                                                            /translation="GFEGKNCELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLA
DNGRAGIFTGGYFGCKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDFTENPFD
LLDFNQTQPEGDNNLTRIVGGGGCKDGECFWQALLNEENEGFGGTILSEEYILTA
AHCLYQAKREEGDRNTEQEEGGEAVHEVEVVIKHNRETKETYDGTGIAVLKTPITFR
MNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLS
SSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGI
        /product="factor X light chain"
205. .1113
                                                                     YTKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK"
                                    /gene="F10"
                                                                                                                                                                               /db_xref-"GDB:G00-119-890"
                                                                                                                                                                                               /protein_id="AAA52486.1"
/db_xref="GI:182821"
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                                                                                                                                                                                                                                          /note="factor x precursor peptide"
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341 c 342 g
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1. .1126
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3.9e-16;
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315 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 374
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                            Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1414)

Kaul, R.K., Hildebrand, B., Roberts, S. and Jagadeeswaran, P.

1 (150) Action and characterization of human blood-coagulation factor:
                                                                                                                               coagulation factor X.

Human liver, cDNA to mRNA, clone pKT218.

Homo sapiens
Gene 41 (2-3), 311-314 (1986)
                                                                                                                                                                                    M22613.1 GI:180335
                                                                                                                                                                                                                   Human blood-coagulation factor X mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kopetzki,E. and Hopfner,K.
RECOMBINANT BLOOD-COAGULATION PROTEASES
Patent: WO 9747737-A 15 18-DEC-1997;
KOPETZKI ERHARD (DE); BOEHRINGER MANNHEIM GMBH (DE)
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Sequence 15 from Patent WO9747737.
A93124
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361. .1113
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402 c 425 q
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MacGillivray,R.T.A.
Unpublished (1985)
2 (bases 3 to 1443)
Fung,M.R., Hay,C.W. and MacGillivray,R.T.
Characterization of an almost full-length cDNA coding for human
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ [ bases 1 to 2 ]
                                                                                                                                        Homo sapiens
                                                                                                                                                blood coagulation factor; factor x.

Human adult liver, cDNA to mRNA, clones pcHX[5,8,14].
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/db_xref="GI:180336"
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Pred. No. 3.8e-16;
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Sequence 43 from Patent W09838318.
A86859 1 GI:6735650
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unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blood coagulation factor x
Proc. Natl. Acad. Sci. U.S.A. 82 (11), 3591-3595 (1985)
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/protein_id="AAA52490.1"
/protein_id="AAA52490.1"
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/db_xref="GI:182841"
/db_xref="GI:182841"
/db_xref="GI:182841"
/db_xref="GI:190-119-890"
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CMEETCSYEEAREVFEDSKTNEFWHKY KOEGOÇCETSPCQNOGKCKOGLGEVTCTCLE
GFEGKNCELFTRKLCSLUNGDCODFCHEEGNSVYCSGARGYTLADNGKACIFTGPNFC
GKQTLERRKRSVAQATSSSGEAPDSITWKFYDAADLDFTENFFDLLDFNQTQPERGDN
MLTRIVGGQECKDGECFWQALLINERMEGFCGGTILSEFYILFARHCLYQAKRFKTWFV
CDRNTTROEEGGEAVHEVVIKHNRFTKETYDDIAVLKTPITFRMNVAPACLPER
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416 c 435 g 231 t
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1117
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AGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGESCARKGKYGIYTKVTAFLKWI
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1467)
Himmelspach,M. and Eibl,J.
FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE
Patent: WO 9838317-A 26 03-SEP-1998;
HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)
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Falkner, F. and Himmelspach, M.
FACTOR X DELETION MUTANTS AND ANALOGUES THEREOF
PATCHET: WO 9838318-A 43 03-SEP-1998;
FALKNER FALKO GUENTER (AT); HIMMELSPACH MICHELE (AT)
LOCATION/Qualifiers
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                 /translation="mgrplhlyllsaslagllllgeslfireoannilarytransfleemkkghlebecmeetcsyeearevfedsdktnefwnkykdddocetspcongkck dglgeytctclegfegknelffrklstdldngcddfecheenksyvcgscargytladn gkaciftgfyeogkotlegfekksvagatssgeapdsitwfydaadldfepedll dfngcdpergyndaadldfepedll dfngcdpergonnltrivgggeekdgecpmqallineenegfoggtilsefyiltaah clygakfkyrgyddntsgegeavhevevikhnrftketydfdadldfytktktpitfklygakrfkyrgdbabstlmigetggeavhevevvikhnrftketydfdiavlrlktpitfkygakrfkyrgdbabstlmigktgfisgegriekekgrgstrlkmleypyudrnsckl
SSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGESCARKGKYG
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LEEMKKGHLERECMEETCSY EELAREVFEDSDKTNEETWIK YKDGDQCETSPCQNQGKCK
DGLGEYTCTCLEGFEGKNCELFTRKLCSLDNGDCDDGFCHEQNGSVCSCARGYTLADN
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CLYQAKREKVRVGDRNTEQEEGGEAV IEVEVVIKHNRFTKFYEDDLAVLRLKTPITF
RMNYAPACLFEEDWAASTLMTQKTG1/SGFGRTIEKGRQSTFIKMLEVPYVDRNSCKL
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SSFIITQNMFCAGYDTKQEDACQGD JGGPHVTRFKDTYFTTGIVSWGESCARKGKYG
TYKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK"
                                                                                                                                                                                            /protein_id="CAB69368.1"
/db_xref="GI:6735678"
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1. .1467
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/db_xref="GI:6735651"
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                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                   ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 458
                                                                                                                                                                                                                                                                                                                                 , 68
                                                                        Wolf
                                              Recombinant agents affecting thrombosis Patent: US 5795863-A 4 18-AUG-1998;
                                                                                                                                                     Sequence 4 from patent US 5795863.
                                                                                             Unclassified.
                                                                                                         Unknown
                                                                                                                      Unknown
                                                                                                                                           AR024194.1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1467)
Himmelspach,M. and Schlokat,U.
Factor x analog with an improved ability to be activated Patent; WO 0110896-A 1 15-FEB-2001;
Baxter Aktiengesellschaft (AT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1 from Patent WOO110896.
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 /organism="unknown"
425 c 441 g
                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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4 424 C 444 G 236 t
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                                                                                                                                         GI:3977488
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Pred. No. 3.8e-16;
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Best Local Similarity 98.9%;
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                                                                                             369 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 428
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                                    71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
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89; Conservative
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Messier, T.L., Pittman, D.D., Long, G.L., Kaufman, R.J. and Church, W.R. Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor x Gene 99 (2), 291-294 (1991)

91216473
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/db_xref="ci:182390"
/db_xref="ci:182390"
/db_xref="ci:182390"
/db_xref="ci:182390"
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/translation="MGRPLHLVLLSASLAGLI.LLGESLFIRREQANNILARVTRANSF
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GKACLFTGPYCCGKOTLERREKSSVAQATSSSGEAPDSITWKPYDADALDLDPTENPPDLL
GKACLFTGPYCCGKOTLERREKSVAQATSSSGEAPDSITWKPYDADALDLDPTENPPDLL
DENOTOPERCONULTRIVGGQECKDGBCPWQALLINEENEGFCGGTILSEFYILTAAH
CLYQAKREKVKYGDRNTEQEEGGEAVBCVVVIKHNRFYKETYDEDIAVLRUTPTF
RMYAPACLPERDWARSTLWTQKTGIVSGGGPHVTRFKDTYFVTGIVSWGEGCARKGKYG
IYTKVTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK"

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(J02459); putative"
429 c 446 g 238 t
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/gene="F10"
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|...1507
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/map="13q34"
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                                                                                                                                                                                                                                                                   88.4%; Score 88.4; DB 9; Length 1507; 98.9%; Pred. No. 3.8e-16;
                                                                                                                                                                                                                                      0; Mismatches
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Db 429 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 458

Search completed: January 15, 2003, 20:35:16 Job time: 1355 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                  January 15, 2003, 17:58:10; Search time 31 Seconds (without alignments) 989.280 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441362 segs, 153338381 residues
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-483-37-4
US-08-469-486-1
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US-09-218-207-184
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US-08-487-427-27
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Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 15, Appl Sequence 15, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 4, Appl Sequence 4, Appl Sequence 18, Appl Sequence 18, Appl Sequence 184, Appl Sequence 182, Appl Sequence 27, Appl Sequence 27, Appl Sequence 182, Appl Sequence 27, Appl Sequence 27, Appl Sequence 182, Appl Sequence 27, Appl Sequence 6, Appl Sequence 6,
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| tch al Sim 89; | Sequence 27, Application to 5877289 Patent No. 5877287 Patent No. 5877287 Patent No. 587288 Patent No. 5872888 Patent No. 58728888 Patent No. 58728888 Patent No. 58728888 Patent No. 5872888888 Patent No. 587288888 Patent No. 5872888888 Patent No. 5872888888 Patent No. 5872888888 Patent No. 58728888888 Patent No. 587288888888888888888888888888888888888 | | 25 55 85 86 86 86 86 86 86 86 86 86 86 86 86 86 |
| h Similarity 89; Conservat | HIT 1 18-479-733A-27 squence 27, Application U teent N. 5877289 ENERAL INCOMPATION: APPLICANT: Thorpe, Phi APPLICANT: Edgington, TITLE OF INVENTION: Sp. NUMBER OF SEQUENCES: 3 COUNTRY: US ZIP: 77210 COMPUTER READLABLE FORM: MEDIUM TYPE: HOUSTON STATE: Texas COUNTRY: US ZIP: 77210 COMPUTER READLABLE FORM: MEDIUM TYPE: Floppy COMPUTER: ISM PC COMPUTER: ISM PC COMPUTER: IT MADER: COUNTRY: US ZIP: 77210 COMPUTER: OF JUPPY COM | | N N N N N N N N N N N N N N N N N N N |
| 88.4 98.9 vative | 1 179-733A-27 179-733A-27 179-733A-27 17 No. 5877289 RRAL IMPORMATION: PPLICANT: Thorpe, Philip E. PPLICANT: Edgington, Thomas it ITLE OF INVENTION: Methods and ITLE OF INVENTION: Specific Compacts: STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: US ZIP: 77210 MPUTER READABLE FORM: MEDIUM TYPB: FIDMPY disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS- SOFTWARE: PATENTIA Release it RRENT APPLICATION NUMBER: US OS/MS- SOFTWARE: PATENTIAN: 424 LIOR APPLICATION NUMBER: US OS/MS- FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 LIOR APPLICATION NUMBER: US 08/27 FILING DATE: 11-JUL-1994 LOR APPLICATION NUMBER: 32,165 REFERENCE/DOCKET NUMBER: 32,165 REGISTRATION NUMBER: 32,165 REGISTRATION SECONMUNICATION: THORWATION: NAME: PATKET, DAVID L. REGISTRATION NUMBER: 32,165 TELEPAN: 512/474-7577 TELEX: N/A TELEPAN: 512/474-7577 TELEX: N/A CHARACTERISTICS: LENGTH: 1126 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear | | 1387 1387 1387 1387 2373 3003 3003 44395 4534 4534 4534 4539 4998 998 |
| de de | Philip E. Philip E. Shilip E. Thomas Methods a Specific 32 32 32 32 32 32 32 32 32 32 32 32 32 | | 0000444440004444 |
| Score 88.4; I Pred. No. 1e-1 0; Mismatches | 3733 S. S. Ind Coa Coa #1. 73, | | US-08-476-866-2 US-08-756-506-3 5270178-1 US-08-980-080-1 US-08-980-080-1 US-09-417-822-6 US-09-417-822-7 US-09-417-822-1 US-09-417-822-1 US-09-417-822-1 US-09-417-822-1 US-09-417-822-1 US-09-417-822-1 US-09-417-823-1 US-09-218-506-1 US-09-318-503-1 US-09-318-503-1 US-09-318-503-1 |
| 88.4; No. 1 | 733A S. Composit Coagulation Coagulation Durkee #1.0, Version 79,733A 79,733A SD:459/PAR | ¥ (| -476-8 -756-5 -756-5 -788-1 -417-8 -417-8 -417-8 -675-5 -675-5 -675-5 -203-9 -203-9 |
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US-08-479-727A-27
; Sequence 27, Application US/08479727A
; Patent No. 6036955
; GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
TITLE OF INVENTION: Methods and C.
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US-08-487-427-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thorpe, running S. APPLICANT: Edgington, Thomas S. APPLICANT: Edgington, Thomas S. TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Specific Coagulation of Vasculature on SEGUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/273,567 FILING DATE: 11-JUN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                         71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                             27 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 86
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Local Similarity 98.9%;
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                    ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 116
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P.O. Box 4433
                                                                                                                                                                                                                                                                                                                       Conservative
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Methods and Compositions for the
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Pred. No. 1e-19;
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RESULT 4
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                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the Specific TITLE OF INVENTION: Coagulation of Vasculature NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32,165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
TELEX: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/273,567
FILING DATE: 11.JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 1126 base pairs
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CORRESPONDENCE ADDRESS:
                                                                                                             COUNTRY: US
ZIP: 77210
                                                                                                                                                                     STREET:
CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: STRANDEDNESS: SIG
                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 116
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les 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parker, David L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/479,727A FILING DATE: 07-JUN-1995
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                                                                                                                                                                     Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                 Texas
                                                                                                                                                                                    E: Arnold, Wh
P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application PC/TUS9507439 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION NUMBER: PC-T/US95/07439
APPLICATION MADER: CONCURRENT APPLICATION MADER: PC-T/US95/07439
FILING DATE: Concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:433/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 1126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                         CITY: Houston
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                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 512/474-7577
                                                                                                                                                                                        ADDRESSEE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/273,567 FILING DATE: 11-JUL-1994
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                                                                                                              77210
                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                            Texas
                                                                                                                                                                        P. C. Box 4433
                                                                                                                             USA
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                                                                                                                                                                                                                                                                                  COUNTRY: Un
POSTAL CODE:
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                                                                                                                                                                                                                                                                                                                                                                                                               POSTAL CODE:
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                                                                                                                                                                                                                                       COAGULATION OF VASCULATURE
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98.9%;
                                                                                                                                                                                                                                                    METHODS AND COMPOSITIONS FOR THE SPECIFIC
                                                                                                                                                                                                                                                                                                California
United States of America
                                                                                                                                                                                                                                                                                                                                             (512)499-4523
THE SCRIPPS RESEARCH INSTITUTE
10666 North Torrey Pines Road
                                                                                                                                                                                                                                                                                                                                                                                                               United States of America DE: 78701
                                                                                                                                                                                                                                                                                                                                LaJolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 West 7th Street Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOARD OF REGENTS, THE UNIVERSITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/482, 369A
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                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version $1.30B (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/202,101
FILING DATE:
INFORMATION FOR SED ID NO: 15:
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                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUN 1994
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTFD433P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Recombinant blood-coagulation proteases NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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375 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 404
                                                               315 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 179-0924
                                                                                                11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
                                  71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
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TELEFAX: (713) 789-2679
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98.9%;
                                                                                                                                      0; Mismatches
                                                                                                                                                      Score 88.4; DB 4;
Pred. No. 1.1e-19;
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                                                                                                                                                                      Length 1404;
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US-08-469-486-1
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TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1500 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08469486 Patent No. 5739281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                             TITLE OF INVENTION: Improved method for the refolding of TITLE OF INVENTION: proteins NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                 APPLICANT: Thoegersen, Hans Christian APPLICANT: Holtet, Thor Las APPLICANT: Etzerodt, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCES: 12
ADDRESS:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         461 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 ATTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 460
                                                                  COUNTRY: USA
ZIP: 02110-2804
                                                                                                   STATE: Massachusetts
                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                         71 ACAGAACTCTGTGGTGTGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGA 70
 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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PC-DOS/MS-DOS
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98.9%;
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Pred. No. 1.1e-19;
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US-08-469-658-1
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TELEFX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRIGTH: 1554 base pairs
                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1,
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                                                                                                                                                                                                                               APPLICANT: Th egersen, I applicanT: Holtet, Thor APPLICANT: Etzerodt, Mid TITLE OF INVENTION: IMPITITLE OF INVENTION: PROVINGER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                             SOFTWARE: Patentin Rel
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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TELEPHONE: 617 542 8906
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FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
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HYPOTHETICAL:
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APPLICATION NUMBER: US/08 FILING DATE: June 5, 1995
                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                             STATE:
                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                      STREET:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 GAACTCTGTGGTGTGCTCCTGCGCCC 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                             , Application US/08469658 5917018
                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                   225 Franklin Street
                                                                                                                                                                                                                                                                                       Holtet, Thor Las
Etzerodt, Michael
                                                                                                                                                                                                                                                                                                                         Th egersen, Hans Christian
                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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76..1551
                                                                                                                                                                                                                  Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                       IMPROVED METHOD FOR THE REFOLDING OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.4%; Score 52.4; DB 1; 75.6%; Pred. No. 4.4e-08;
                US/08/469,658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/469,486
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                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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CLASSIFICATION: 530 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/192,060 FILING DATE: February 4, 1994

February 4, 1994 N: 530

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US-08-282-141-1
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TELEX: 200154
TELEX: 200154
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-469-658-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08282141 Patent No. 5538861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                 CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                        COMPUTER REA ABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Schneider, Claudio
APPLICANT: Varnum, Brian
APPLICANT: Avanzi, Giancarlo
APPLICANT: Brancolini, Claudio
APPLICANT: Manfioletti, Guidalberto
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507 CAGCGAGGTGCGGCTGCTGCGCGC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                              STREET: 1840 Dehavil
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                    COUNTRY: United States ZIP: 91320-1789
                                                                      FILING DATE:
                                                                                   APPLICATION NUMBER:
   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GAACTCTGTGGTGTGCTCCTGCGCCC 99
                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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2461 base pairs
                                                                                                                                                                                                                                                                    1840 Dehavilland Drive
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA
                                                                                                                                                                                                                                                                                                                                     Stimulating Factor for the AXL Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.4%;
75.6%;
                                                                                   US/08/282,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.4; DB 2; Length 1554;
Pred. No. 4.4e-08;
0; Mismatches 21; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-453-702B-251
                                                      Best Local Similarity 61.6
Matches 45; Conservative
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 251, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 251
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
18 CGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGAAGAACAGAAC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            612 TGCAGCCAGGAGAACGGGGGCTGCCTCCAGATCTGCCACAACAAGCCGGGTAGCTTCCAC 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 TGTTCCTGCCACAG 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 TGCTCCTGCGCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 TGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGAACAGAACTCTGTGGTG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 251:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORD Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 960296.95017 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch.
                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  TELEPHONE: (608)
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                  LENGTH: 22306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :ITY: Madison
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Plunkett, v.,
Plunkett, v.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burland,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 South Pinckney Street
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                                                                     28.2%;
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                                                                                                                                                                                                                                                                   251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guy
                                                    0; Mismatches
                                                                Score 28.2; DE Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valerie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30.8; DB Pred. No. 0.44;
                                                                               DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.44Mb storage
                                                    28;
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                                                                                 Length 22306;
                                                  Indels
                                                 0;
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16880 CTGATGCGCTTCGGGCTGACCATCCGGAACTGTGTCCGGAACAGTCGCGAGGGACGGGTA 16939

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                                                                          RESULT 13
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; Sequence 72, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                Sequence 2, Application US/09103840A Patent No. 6294328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                 15048 TCCCAGGTGGCCT 15036
                                                                                                                                                                                                       15108 CTGATGCGCTTCGGGCTGACCATCCGGAACTGTGTCCGGAACAGTCGCGAGGGACGGGTA 15049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16940 TCCCAGGTGGCCT 16952
                                                                                                                                                                       78 TCTGTGGTGTGCT 90
                                                                                                                                                                                                                            18 CGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTCTGCCACGAGGAACAGAAC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGISTRATION NUMBER: 960296.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 TCTGTGGTGTGCT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 46819
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1 South Pinckney Street CITY: Madison
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                                                                                                                                                                                                                                                                                      Conservative
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Burland,
Nicole T.
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61.6%;
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Pred. No. 6.3;
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                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   960296.95017
                                                                                                                                                                                                                                                                                    28; Indels
                                                                                                                                                                                                                                                                                                                        Length 46819;
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                                                                                                                                                                                                                                                                                Gaps
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Db 3922204 TTGGGAATCGCACCGGATATCTTCGACCTGGACGACGACGACTATGCCGTGGTC 3922151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 3915983 TTGGGAATCGCACCGGATATCTTCGACCTGGACGACGACGACTATGCCGTGGTC 3915930
GENERAL INFORMATION:
APPLICANT: Kelly, Kathleen
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods and Compositions for Inhibiting
TITLE OF INVENTION: and Anglogenesis Comprising a Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-840A-2
                                                                                                                                                                          Sequence 8, Application US/09284819
Patent No. 6365712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILLMG DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: YENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or {\bf g}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                           26.8%;
Local Similarity 68.5%;
les 37; Conservat'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TIGGCAGTCACACGGAAGCTCTGCAGCCTGGACAACGGGGACTGTGACCAGTTC 59
                                                                                                                                                                                                                                                                                                                                                           6 TIGGCAGICACACGGAAGCICIGCAGCCIGGACAACGGGGACIGIGACCAGIIC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26.8;
Pred. No. 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26.8;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 4403765
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       Inflammation CD97 Alpha
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FILE OF INVENTION: Subunit
FILE REFERENCE: 015280-253100US
CURRENT APPLICATION NUMBER: US/09/284,819
CURRENT FILING DATE: 1999-08-20
EARLIER APPLICATION NUMBER: US 60/027,871
EARLIER FILING DATE: 1999-08-20
LEARLIER FILING DATE: 1999-08-20
LEARLIER FILING DATE: 1999-08-20
LEARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOW: 21
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: OF SEQ ID NOS: 21
CHARTH: 3156
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
ORGANISM: Homo sapiens
FEATURE:
ORGANISM: Homo sapiens
FEATURE:
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: CD97
J-09-284-819-8
OUCATION: (49)..(2556)
OTHER INFORMATION: CD97
J-09-284-819-8
OUCATION: 48: CONSERVATIVE 0; Mismatches 36: Indels 0; Gaps
Matches 48: Conservative 0; Mismatches 36: Indels 0; Gaps
Matches 48: Conservative 0; Mismatches 36: Indels 0; Gaps
OV 17 ACGGAAGCTCTGCAGCCTGGACAACGTGGAACCTCTGCCCGGCCAGGGAACAGAA 76
Db 3093 ACACAACCTCTACAACCTTCACAACAGTGAAACCTCTGCCCGGCCAGGGAACAGGC 3034
OV 77 CTCTGTGGTGTCTCCTGCCCCGG 100
Db 3033 CTCTGTACCGTGAGCCTCAGGCCAGGGAACGTC 3034
Search completed: January 15, 2003, 20:51:13
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0;

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tal number of hits satisfying chosen parameters:
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                           Score
                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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Match
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   34.2
34.2
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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   2063
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2063
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396
420
1674
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 9 US-09-808-602-100

US-09-764-898-72

9 US-10-063-547-111

9 US-10-174-590-329

US-10-176-758-329

US-10-06-867-121

12 US-10-052-586-329

10 US-09-851-588-7

10 US-09-851-588-7

10 US-09-960-352-10052

10 US-09-960-352-10052

10 US-09-981-626-1340

10 US-09-738-626-1340

10 US-09-755-016-5

10 US-09-755-016-5

10 US-09-755-016-5

10 US-09-755-016-5

10 US-09-755-016-7

10 US-09-755-016-7

10 US-09-888-615-5863

10 US-09-755-016-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Search time 32.5 Seconds
(without alignments)
1371.902 Million cell updates/sec
Sequence 100, App
Sequence 72, Appl
Sequence 329, App
Sequence 111, App
Sequence 7, Appl1
Sequence 7, Appl1
Sequence 1340, App
Sequence 1340, App
Sequence 3, Appl1
Sequence 3, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 5, Appl1
Sequence 7, Appl1
Sequence 7, Appl1
Sequence 3, Appl1
Sequence 3, Appl1
Sequence 3, Appl1
                                                                                                                                                                                                                                                                                                                          Description
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| | 2555 | 25.8 | 25.8 | 45 | |
|-----------------------|-------|------|------|--------|---|
| 10 US-09-880-107-2256 | 2493 | 25.8 | 25.8 | 44 | |
| 9 US-09-808-602-92 | 2386 | 25.8 | 25.8 | 43 | |
| 10 US-09-925-302-169 | 2063 | 25.8 | 25.8 | 42 | |
| 9 US-10-078-770-91 | 681 | 26.0 | 26 | 4 | O |
| 9 US-10-047-542-14 | 8074 | 26.2 | 26.2 | 40 | |
| 9 US-10-047-542-101 | 7129 | 26.2 | 26.2 | 39 | |
| 9 US-09-981-353-58 | 3149 | 26.2 | 26.2 | 38 | |
| 9 US-09-989-919-74 | 2919 | 26.2 | 26.2 | 37 | |
| 9 US-09-982-107-3 | 2919 | 26.2 | 26.2 | 36 | |
| 9 US-10-047-542-12 | 1845 | 26.2 | 26.2 | ω U | |
| _ | 1839 | 26.2 | 26.2 | ω 4 | |
| 9 US-09-147-947-3 | 2614 | 26.4 | 26.4 | ω ω | |
| 9 US-09-147-947-5 | 2562 | 26.4 | 26.4 | 32 | |
| | 1543 | 26.6 | 26.6 | 31 | |
| 10 US-09-888-615-32 | 987 | 26.6 | 26.6 | 30 | |
| 10 US-09-728-446-1164 | 224 | 26.6 | 26.6 | 29 | |
| 10 US-09-822-849A-158 | 857 | 26.8 | 26.8 | 28 | |
| 9 US-10-013-310-4 | 3286 | 27.8 | 27.8 | 27 | |
| _ | 38059 | 28.0 | 28 | 26 | |
| g | 32193 | 28.0 | 28 | 25 | o |
| 10 US-09-764-847-1550 | 32187 | 28.0 | 28 | 24 | o |
| ā | 2792 | 28.0 | 28 | 23 | |
| 10 US-09-841-880-1 | 1937 | 28.0 | 28 | 22 | a |
| 10 US-09-150-811-6 | 1548 | 28.0 | 28 | 21 | |
| 10 US-09-884-901-2 | 1413 | 28.0 | 28 | 20 | |
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ALIGNMENTS

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SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 100
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo sapiens
US-09-808-602-100
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US-09-808-602-100
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Best Local S
Matches 54
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 100, Application US/09808602 Patent No. US20020155115A1
                                                                                                                                                                                                                                                                   APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-03
NUMBER: 05 SEQ ID NOS: 114
NUMBER OF SEQ ID NOS: 114
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                            · 77 TCCTAACGCCAGCCCACTGTCTCT 100
267 TCCTCACCGTGGCCCACTGCTTCT 290
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                                                                                                                         Local Similarity nes 54; Conserv
                                                                           TGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAGCCATTCTGAGCGAGTTCTACA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                Fernandes, Elma
Shimkets, Richard A
Herrman, John L
Majumder, Kumud
Mishra, Vishnu
Mezes, Peter S
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                                                                                                                           Conservative
                                                                                                                                    36.0%;
                                                                                                                                      Score 36; DB 9;
Pred. No. 0.00054;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-72
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                                                                                                                                                Matches
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                            SEQ ID NO 11:
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Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US20020182638A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 111, Application US/10063547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 72
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                                                                                          Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
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                                                                                                                                                                                                                                                                           LENGTH: 2063
917 CACGGCAGCCCACTGCTTC 935
                                                               857 CATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCT 916
                                  81 AACGGCAGCCCACTGTCTC 99
                                                                                    21 CATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCAT TTGAGGCGAGTTCTACATCCT 80
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                                                                                                                                                             Local Similarity
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Local Similarity 64.68;
nes 51; Conservarior
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                                                                                                                                            51; Conservative
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                                                                                                                                                             64.68;
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                                                                                                                                        0; Mismatches
                                                                                                                                                      Score 34.2; DB 9; Length 2.63; Pred. No. 0.0034;
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Pred. No. 0.0032;
0; Mismatches 28;
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                                                                                                                                        Indels
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RESULT 4

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; Prior Application removed - See File Wrapper or Palm NUMBER Cr SEQ ID NOS: 612 ; SEQ ID NO 329 ; ERUCH: 2063 ; TYPE: DNA ; ORGANISM: Homo Sapien US-10-176-758-329
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US-10-176-758-329
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-329
Query Match
Best Local Similarity 64.6
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 329,
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030008353A1
                                                                                                                                                                                        FILE REFERENCE: P3430RIC104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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Best Local Similarity
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                                                                                                                                                                                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin p. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C42
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                                                                                                                                                                                                                                                                                                                                                                                   Godowski,Paul
                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
                                                                                                                                                                                                                                                                                               Watanabe,Colin K. Wood,William I.
                                                                                                                                                                                                                                                                                                                                 Smith, Victoria
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                         34.2%;
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   Score 34.2; DB 9; Length 2063; Pred. No. 0.0034; 0; Mismatches 28; Indels 0.
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RESULT 6
US-10-006-867-111
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APPLICANT:
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APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                             PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR
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CURRENT FILING DATE: 2001-12-06
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DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088811
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088824
DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088825
DR FILING DATE: 1998-06-10
DR FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR APPLICATION NUMBER: 60/088029
OR FILING DATE: 1998-06-04
OR FILING DATE: 1998-06-04
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088734
OR FILING DATE: 1998-06-10
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                       APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090688
                                                                                                                     APPLICATION NUMBER: 60/
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/085579
FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/088863
FILING DATE: 1998-06-11
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083495
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FILING DATE: 1997-10-29
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         1998-06-25
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FILING DATE: 1998-10-06
APPLICATION NUMBER: 60/103678
FILING DATE: 1998-10-08
                                                                                         APPLICATION NUMBER: 60/105002
FILING DATE: 1998-10-20
APPLICATION NUMBER: 60/105881
FILING DATE: 1998-10-27
FILING DATE:
APPLICATION |
                                                     APPLICATION NUMBER: FILING DATE: 1998-10
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FILING DATE: 1998-09-24
               APPLICATION NUMBER: 60/106464 FILING DATE: 1998-10-30
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FILING DATE: 1998-10-08
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FILING DATE: 1998-09-24
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FILING DATE: 1998-08-18
APPLICATION NUMBER: 60/0
FILING DATE: 1998-08-26
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FILING DATE: 1998-09-23
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FILING DATE: 1998-09-17
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APPLICATION
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FILING DATE: 1998-09-10
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FILING DATE: 1998-09-01
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FILING DATE: 1998-08-26
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FILING DATE: 1958-08-17
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 50/091628
FILING DATE: 1998-07-02
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FILING DATE: 1998-06-25
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60/106030

60/105000

60/101743

60/101916

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                                                         Matches
                                                                             Best
                                                                                           Query Match
21 CATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTCTGAGCGAGTTCTACATCCT 80
                                                                           Local
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FILING DATE: 1998-12-30
APPLICATION NUMBER: 60/115614
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APPLICATION NUMBER: 60/113011
FILING DATE: 1998-12-16
                                                                                                                               APPLICATION NUMBER: 09/380142
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380137
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FILING DATE: 1999-12-07
APPLICATION NUMBER: 60/175481
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APPLICATION NUMBER: 60/108807
FILING DATE: 1998-11-17
APPLICATION NUMBER: 60/112419
FILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/380139
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FILING DATE: 1999-04-27
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APPLICATION NUMBER: 60/129122
FILING DATE: 1999-04-13
APPLICATION NUMBER: 60/129674
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FILING DATE: 1999-02-10
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APPLICATION NUMBER: 60/119287
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APPLICATION NUMBER: 60/116527
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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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FILING DATE: 1997-12-11
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APPLICATION NUMBER: 60/066466
FILING DATE: 1997-11-24
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                                       APPLICATION NUMBER: 60/069870 FILING DATE: 1997-12-17 APPLICATION NUMBER: 60/068017 FILING DATE: 1997-12-18
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FILING DATE: 1997-12-12
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APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-10
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NUMBER: 60/089908
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; OTHER INFORMATION:
US-09-851-588-7
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Best Local
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Query Match
Best Local Similarity
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APPLICANT: Gish, Kurt C.
APPLICANT: Wilson, Keith E.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
FILE REFERENCE: A-68829-1/DJB/JJD/AMS
CURRENT APPLICATION NUMBER: US/09/851,588
CURRENT FILING DATE: 2001-09-24
CURRENT FILING DATE: 2001-09-24
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PRIOR FILLING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: US 09/656,002
PRIOR FILLING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 9
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PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: US 09/656,002
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TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS FILE REFERENCE: A-68829-1/DJB/JJD/AMS
CURRENT APPLICATION NUMBER: US/09/851,588
CURRENT FILING DATE: 2001-09-24
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NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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34.2%;
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Pred. No. 0.0034;
0; Mismatches 28;
  Score 34.2; DB 10;
Pred. No. 0.0034;
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; OTHER INFORMATION: Clone ID: 43-LIB34-017-Q1-E1-C4
US-09-960-352-10052
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FILE REFERENCE: 16511.06/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 10052
LENGTH: 396
Type: Num
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US-09-960-352-6361
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SEQ ID NO 6361
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                        Query Match
Best Local Similarity
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION ANI
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
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                                                                                                                LENGTH: 420
TYPE: DNA
ORGANISM: Bos taurus
                                                                                                  OTHER INFORMATION: Clone ID: 27-LIB34-043-Q1-E1-G3
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Score 30.2; DB 10,
Pred. No. 0.057;
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LENGTH: 1674
TYPE: DNA
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Patent No. US20020064856A1
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              APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
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APPLICANT: WHYTE, DAVID
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
SOFTWARE: PatentIn Ver. 2.1
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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CHARYDCZAK, GLEN
MANNING, GERARD
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TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.8%; Score 29.8; DB 9; Length 1674; 66.2%; Pred. No. 0.14; tive 0; Mismatches 22; Indels 0.
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; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-755-016-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-755-016-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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; ORGANISM: Homo sapiens
US-09-888-615-36
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; LENGTH: 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/174,686
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 867
                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09755016 Patent No. US20010034437A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09755016 Patent No. US20010034437A1 GENERAL INFORMATION:
                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity 70.4%;
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 44; Conservative
                                                                                                                                                                                   APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20010034437A1el Human Proteases and Polynucleotides Ency
FILE REFERENCE: LEX-0114-USA
CURRENT APPLICATION NUMBER: US/09/755,016
CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20010034437A1el Human Proteases and Polynucleotides Ency
FILE REFERENCE: LEX-0114-USA
CURRENT APPLICATION NUMBER: US/09/755,016
CURRENT FILING DATE: 2001-06-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 AAGTGAACCTTTCTGTGGCGGCTCCATCCTCAACAAGTGGTGGATTCTCACTGCGGCTCA 323
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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1277.247 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est2:*
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| вм646546 | ĭ | 5 | 1400 | οŪ | BG288427 | BQ92200 | CNS04KQI | BM686292 | 37 | BG984172 | AL694581 | BF896867 | AI258617 | BJ493141 | BQ790628 | AK016601 | AI526776 | AI893715 | AA140046 | AL835455 | BG641885 | BG641612 | BG641571 | AA554502 | BM438664 | AI192868 | CNS039FM | CNS02TO1 | AL553470 | AA237419 | BI144826 | W70579 | W70576 | BG609107 | AL521984 | 5 | AL570383 | 77 |
| вм646546 170006873 | DAUGUOU INTELLEG | ALZ31421 Tetraodon | T. PTIL CANONING | BCCC4855 Homo Sapt | BG28842/ 602388091 | BESIDE AGENCOURT | AL295155 Tetraodon | | AI158537 ud25e02.r | BG984172 IL5-CN006 | AL694581 AL694581 | BF896867 PM3-MT011 | AI258617 LP01850.5 | вJ493141 вJ493141 | BQ790628 92-M3-272 | AK016601 Mus muscu | AI526776 uj42g03.y | AI893715 mr73h12.y | AA140046 mr73g12.r | AL835455 AL835455 | BG641885 pgl1c.pk0 | BG641612 pgllc.pk0 | BG641571 pgllc.pk0 | AA554502 n136e02.s | BM438664 IpLvr0126 | | _ | AL213418 Tetraodon | AL553470 AL553470 | AA237419 mx19d10.r | BI144826 602910055 | ₹ | W70576 me42a04.rl | 9 | ä | AL521983 AL521983 | ü | |

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|--|--|---|--|--|
| | FEATURES source | REFERENCE AUTHORS TITLE JOURNAL COMMENT | ACCESSION VERSION KEYWORDS SOURCE ORGANISM | RESULT 1 AL570367/C LOCUS DEFINITION |
| /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSODIO20YH13" /clone="LTD="LTPLO06_PL2" /tissue_type="placenta" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end | Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers 1 .855 | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 855) 1.(When to | prime, mRNA sequence. AL570367 AL570367.1 GI:12926604 EST. human. Homo sapiens | AL570367 HIL_NFL006_PLZ HOMO Sapiens CDNA clone CSODIO20YH13 3 |

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BASE COUNT
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AL576464/c
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                                           62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL576464.1 GI:12938633
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                                                                                                                                                                                                                                                                                                         /note-Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco RV sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: flang@lifetech.com URL:
                                                                                                                                                                                                                                                                   http://fulllength.invitrogen.com"
1 251 c 239 g 188 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI076YA10"
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263 c 250 g 210 t
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ye76a02.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-IL3-NTO105-200
700-220-A03&t3-2000-07-20&t4-1)
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1 (bases 1 to 246)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: puc 18 forward
High quality sequ nce stop: 246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note**Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTRE PER (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.*
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/clone_lib="NTO105"
/dev_stage="Adult"
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1 (bases 1 to 329)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
Homo sapiens
                                                AV694819.1
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Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 814
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/clone="IMAGE:123626"
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/sex="male"
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/db_xref="GDB:476171"
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                         1 (bases 1 to 1049)
NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene
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Chinese National Hum
                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 86-21-508019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 Guo Shoujing Road,
                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
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/dev_stage-"Adult"
/lab_host="SOLR"
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/clone_lib="GKC"
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Pred. No. 4.4e-21;
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e column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          855 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags of 280,000 human expressed sequence tags of 280,000 human expressed sequence tags
                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 840 Std Error: 0.00
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                                                                                                                                                                                   Seq primer: reverse ET
                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N77287 479 bp mRNA linear EST 28-JAN-1997 yv43:002.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:245474 5' similar to gb:M57285 COAGULATION FACTOR X PRECURSOR
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                   /organism="Homo sapiens"
/db_xref="GDB:3794720"
/db_xref="taxon:9606"
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/clone-"IMAGE:245474"
                                                                                                                           Location/Qualifiers
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/clone_lib="NIH_MGC_125"
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/db_xref="taxon:9606"
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92.9%;
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Pred. No. 1.3e-20;
0; Mismatches 7;
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y Match 81.6%;
Local Similarity 95.0%;
hes 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 984)
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                                                                                                                   /tissue_type="placenta"
/note="Vector: pCNVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcNVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                     http://fulllength.invitrogen.com"
269 c 300 g 160 t
                                                                                                                                                                                                                                                                                                          /clone="CSODIO20YH13"
/clone_lib="LTI_NFLO06_PL2"
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/db_xref="taxon:9606"
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97.88;
             Score 81.6; DB 9;
Pred. No. 3.4e-18;
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Pred. No. 1.9e-20;
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AL521983/c
                                                                          DEFINITION
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                                                                                                                                                                                                                                                                     2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGT-GGTGGAACCATT 60
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                              94;
 AL521984.1 GI:12785477
EST.
                                                                    AL521984 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB007YC01 5
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1 (bases 1 to 820)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                  http://fulllength.invitrogen.com*
222 c 260 g 184 t 3
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/db_xref="taxon:9606"
/clone="CS0DB007YC01"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                             Score 80; DB 9; Lenglu v.v.,
Pred. No. 1.1e-17;
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sapiens cDNA clone CSODBOO7YCO1 3
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                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 521)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                      Email: smith@email.marc.usda.gov
                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                               Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                 Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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                                                                                                                                                                                                                                     discovery in swine
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/lab_host="DH10B"
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/clone_lib="LTI_NFL004_NBC2"
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93.9%;
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Pred. No. 2.7e-17;
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Best Local Similarity
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                                                                                                                                                                                                                      MGI:241958
Seq primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 609)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   me42a04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:390126 5' similar to gb:M57285 COAGULATION FACTOR X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 97 row: M column: 13
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
164 c 182 g 64 t
                                       /db_xref="taxon:10090"
/clone="IMAGE:390126"
/clone_lib="Soares mouse
                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
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/tissue_type="embryo"
                       /sex="unknown"
                                                                                                                                                                          ocation/Qualifiers
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86.7%;
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NbME13.5 14.5 Mus musculus cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w/U5/9
617 bp mRNA linear EST 17-JUN-1996
me42b03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:390125 5' similar to gb:M57285 COAGULATION FACTOR X
                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortiva (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 617)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                     Seq primer: ETF1imer
                                                                                                                                                                                                                        MGI:241957
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone="IMAGE:390125"
/clone_lib="Soares mouse
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
                                                                                                           /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                 1. .617
                                       /sex-"unknown"
                                                                                                                                                                  Location/Qualifiers
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/lab_host="DH10B"
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78.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64.4; DB 14;
Pred. No. 3.7e-12;
0; Mismatches 21;
                                                    embryo NbME13.5 14.5"
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  Query Match
Best Local Similarity
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nes 77; Conserva+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI1139 row: m column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus l (bases l to 824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI144826 824 bp mRNA linear EST 05-JUL-20 602910055F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5051317 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI144826.1 GI:14604827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                  /db_xref="taxon:10090"
/dlone="IMACE:5051317"
/clone="IMACE:5051317"
/clone="IMACE:5051317"
/clone="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-re;istant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally, Primer: Oligo dT.
/site_2: SalI; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 1.9 %b. Constructed by Life
Technologies, Note: this is a NCI_CGAP Library."
a 204 c 248 g 160 t
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                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="FVB/N"
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78.6%;
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Score 64.4; DB 13; Pred. No. 4.3e-12;
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74 ACATCCTAACGGCAGCCCACTGTCTC 99

1 CTCTGCTCATTAACGAAGACAATGAAGGGTTCTGTGGGGGGCACCATCTTGAATGAGTTCT 60

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                                                        Matches
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14 CCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTCTGAGCGAGTTCT 73
                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is av ilable royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                       Similarity
                                                                                                                                                             147 a
                                                   Conservative
                                                                                                                                                                            constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                     double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                           /clone_lib="Soares ...ouse NML"
/tissue_type="Liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:680659"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                     58.8<del>8</del>;
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                                            Score 58.8; DB 9;
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Db 61 ACATCCTCACTGCCCCACTGTCTC 86

Search completed: January 15, 2003, 21:18:51 Job time: 1272 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 0000 2000 2000 2000 2000 2000 2000 200 | 0 115 115 117 117 118 118 118 118 118 118 118 118 | . 1111111111111111111111111111111111111 | Result |
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| 377 377 377 377 377 377 377 377 377 377 | | 9922.6644 9922.6649 9922.6649 | Score |
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| AC129457 GPIFIXA RATFIXA MUSFIXA AX250084 MUSFIXA MUSFIX AL671984 AL671984 AL672083 AY118979 AC000389 AC0003994 AE0003721 | A86859 A86886 AX08259 AX0824194 HUMFACX AF211347 AC127308 AMC0AGULX BTCEXI BTCEXI BTCEXI BTGEXI BTGEXI BTGEXI AT3583 AR001423 BC0032877 AF003200 AF519546 AF7575654 AR0129680 AR1129680 | HUMEX7 AL137002 AF503510 AF503510 AR121387 AR121387 AR12419 AX022601 E36142 E36142 E36142 E36142 E36142 HUMEX HUMEX HUMEX HUMEX HUMEX HUMEX HUMEX HUMEX HUMEX | ID |
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| AC129457 Rattus no M26237 Guinea pig M26247 Rat factor M26236 Mouse facto AX250084 Sequence M23109 Mouse coagu AL6712984 Mus muscu AL672083 Zebrafish AX118979 Drosophil AC0020389 Drosophil AC0003994 Drosophil AC0003994 Drosophil AC0003994 Drosophil | Sequence Sequence Sequence Sequence Sequence 47 Mus 8 8 Mus m 8 Mus m 8 Mus m 9 Roylne Sequence 3 Sequence 77 Mus 10 Oryct 6 Danic 6 Danic 70 Rattu | Human 102 Huma 103 Huma 104 Home 105 Sequ 105 Sequ 106 Sequ 106 Sequ 106 Sequ 107 Human 108 Human 108 Human | Description |
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ALIGNMENTS

| REFERENCE | ORGANISM | SOURCE | SEGMENT | KEYWORDS | VERSION | ACCESSION | DEFINITION | LOCUS | HUMF'X7 | RESULT 1 |
|---|-------------------|---|-------------------------|--|--------------------|---------------|---|--|---------|----------|
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 142) | DNA. Homo sapiens | Homo sapiens (tissue library: of Lawn et al., and Yoshitake et al.) | serine protease. 7 of 8 | Stuart factor; blood coagulation factor; factor X; glycoprotein; | L00396.1 GI:182828 | L00396 M14327 | Human factor X (blood coagulation factor) gene, exon 7. | HUMFX7 142 bp DNA linear PRI 09-NOV-1994 | | |

Pred. No.

is the number of results predicted by chance to have a

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COMMENT
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requests: clonerequest@sanger.ac.uk
On May 8, 2001 this sequence versicn replaced gi:13274222.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >-
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CTGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                                                                                                                                  Submitted (04-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA sequence from clone RI 13q22.1-31.1, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 a 35 c 38 g 31 t about 3.4 kb after segment 6; chromosome 13q34.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL137002.19 GI:13990998
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join(L00390.1:1. .95,L00391.1:1. .185,L00392.1:1.
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.9037 .9002

copies 17 mer 95% copies 26 mer /note-"

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5 copies 9 mer cccgaaccc 63% conserved*

copies 18 mer 81% conserved copies 51 mer 93% conserved" copies 38 mer 98% conserved*

9059

copies 35 mer 75% conserved*

69% conserved conserved.

copies 28 mer 83% conserved*

note="3 copies 18 mer 90% conserved" 9427. 9530 "note="4 copies 26 mer 92% conserved" 10204. .10602

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IMPORFANT: This sequence is not the entire insert of clone RP11-98F14 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-98F14 is at 1 in this sequence true left end of clone RP11-39JH12 is at 132834 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr13
RP11-98F14 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; TT:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The true right end of clone RP11-265C7 is at 123923 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database can be found at
                                                                                                          6565
/note-"2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"AluSq repeat: matches 1. .307 of consensus"
                                                                                                                                                                                                    /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER58A repeat: matches 19. .167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CpG island"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="AluJo repeat: matches 1. .229 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-98F14"
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                                                                                                                                                               .6563
                                    "3 copies 35 mer 85% conserved"
.6687
                                                                                                                                                                                                                                                                                                                  38 copies 16 mer 78% conserved"
                                                                                                                                                                                                                                                                                                                                                                       11M3e repeat: matches -118. .34 of consensus
                                                                                                                                                                                                                                                      .9 copies 32 mer 87% conserved
                                                                                                                              copies 51 mer 93% conserved"
                                                                                                                                                                                          copies 38 mer 93% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies 32 mer 93% conserved*
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/note="9 copies 30 mer 61% conserved"
31153. .31267
/note="Single clone region. Sequence from reads from short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="7 copies 57 mer 87% conserved"
11050. .11091
/note="2 copies 21 mer 100% conserved"
11469. .11823
/note="LLMC1 repeat: matches 5862. .6231 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1M4 repeat: matches 3686. .4029 of consensus" 25311. .25620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSq repeat: matches 1. .304 of
27585. .27688
/note="4_copies 26 mer 74% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16956. .17159
/note="4 copies 51 mer 95% conserved"
19411. .19587
                                                                                                                                                                                                                                    terminator reads only.
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25000. .25306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="5 copies 70 mer 82% conserved"
15491. .15973
                                                                                                                                                        note="13 copies 26 mer 62% conserved"
                                                                                                                                                                                                                                          /note="Sequence from uni-directional dGTP big dye
terminator reads only."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LTR5 repeat: matches 690. .733 of consensus"
13806. .14155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluSx repeat: matches 1. .309 of consensus"
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l6. .21894
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1. .29498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="3 copies 59 mer 79% conserved"
                                                                                                                                                                                                                                                                                                                                 e="14 copies 32 mer 61% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="AluY repeat: matches 1.
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REFERENCE
AUTHORS
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DEFINITION
ACCESSION
VERSION
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ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTTGGTGGAACCATT 72069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 72109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens coagulation factor X (F10) gene, complete cds. AF503510
AF503510.1 GI:20336667
                                                                                                                                                                                                                                       Direct Submission
Submitted (17-APR-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: SeattleSNPS. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).
                                                                                                                                                                                                                                                                                                                                          Rieder, M.J., Armel, T.Z., Carrington, D.P., Chung, M.-W., L
Ozuna, M., Poel, C.L., Toth, E.J., Yi, Q. and Nickerson, D.A.
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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/note="6 copies 32 mer 64% conserved"
32271. 32535
/note="5 copies 52
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/note="12 copies 21 mer 61% conserved"
31268. .31411
/note="9 copies 16 mer 64% conserved"
/frequency="0.01"
/replace="a"
577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="2 copies 35 mer 92% conserved" 33336. .33475 /note="4 copies 35 mer 70% conserved" 33367. .33893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31896. .35863
/note="CpG island"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="21 copies 51 mer 89% 31884. 32937 /note="62 copies 17 mer 89%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Tandem repeat. Forced join. Gap size estimated be approximately 350bp by restriction digest data."
                                                                                                        /replace="c"
167
                                                                                                                                                                                                                       Location/Qualifiers
                                                                frequency="0.01"
replace="t"
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                                                                                                                                                                                        /organism-"Homo sapiens"
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Pred. No. 3.5e-24;
); Mismatches 0;
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| variation | | variation | variation | | | | | | CDS | mRNA | gene | | variation | variation | | variation | variation | Aditacion | ; ; ; ; ; | repeat_region | variation | variation | • | variation | variation | variation | A 01 1 0 1 10 11 | | variation |
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| 2456 /gene="F10" | /gene="F10" /frequency="0.22" /replace="g" | /gener riv /frequency="0.01" /replace="t" 2011 | 1110 101 101 101 100 100 100 100 100 10 | CLYQAKKEKYKGURWIEQEEGEAWHE/EVYLKHNRFTKET/DFDLAYLRUKTPITE RMNVAPACLPERDWAESTLMTQKTGIVS:FGRTHEKGRQSTRLKMLEVPYVDRNSCKL SSSFIITQNMFCAGYDTKQEDACQDSG:PHVTRFKDTYFVTGI/SWGEGCARKGKYG TVTXTTA ET MAT DERWEBGI DE AGGIA DE VTTGCTIVE | GKACIPTGPYPCGKQTLERRKRSVAQATSSSGEAPDSITMKYDAALLDPTENPFDLL DFNQTQPERGDNNLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAAH | /W_ALEL- G. 100000000000000000000000000000000000 | /product="coagulation factor x" /protein_id="AAM19467.1" | 22912,2619826315,27735 | /product="coagulation factor x" join(16721741,82698429,1727417298,1817418287, | Join(<.16471741,82698429,1727417298,1817418287, 1973619867,2266822912,2619826315,2773528346) /qene="F10" | 46 | /frequency="0.01" /replace="t" | /replace="a" 1632 | 1612 /frequency="0.01" | /frequency="0.33" ./replace="a" | /replace="c" /replace="c" | /frequency="0.48" | /frequency="0.57" /replace="" | σ | /replace="a" 1189. 1395 | 1169 /frequency="0.02" | /frequency="0.79" /replace="" | /frequency="0.05" /replace="c" | /irequency="0.02" /replace="a" 800 | /replace="g" | 851 /frequency="0.01" | /frequency="0.12" /freqlace="c" | frequency="0.01" | /frequency="0.33" /replace="t" |
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| | variation | variation | variation | • | variation | misc_feature | variation | | variation | variation | | variation | repear_regrou | 1 | | variation | | variation | variation | | variation | | variation | repeat_region | misc_feature | | variation | 741 14 14 14 14 | variation |
| /gene="F10" /frequency="0.06" | /yene= riv /frequency="0.01" /replace="c" 6445 | /irequency="0.03" /replace="a" 6110 | /gene="F10" | /gene="F10" /frequency="0.01" /replace="c" | <pre>/gene="flu" /note="Region not scanned for variation" 5997</pre> | /frequency="0.11" /replace="a" 55405950 | /gene="F10" | /gene="F10" /frequency="0.13" | N. | 5300 /gene="F10" /fremmonve="0 00" | /frequency="0.01" /replace="q" | S128 | /rpt_fomily="L2" /rpt_fomily="L2" /rpt t_op=dispersed | /replace="c" /replace="c" /ser /oer | /gene="F10" /frequency="0 19" | /requency="0.01" /replace="t" 4544 | /gene="F10" | /frequency="0.01" /replace="c" 4100 | 3977 /gene-"F10" | /frequency="0.39" /replace="q" | 740 Johnsengion | /gene="F10" /frequency="0.09" /replace="t" | /rpt_type=dispersed 3715 | /note="Region not scanned for variation" 3544. 3975 | 28603410 /gene="F10" | /frequency="0.04" /freplace="q" | /replace="c" 2757 //ene="#10" | /gene="F10" /frequency="0.12" | /frequency="0.04" /replace="a" 2527 |

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                                                                  65 GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 124
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725 bp
Sequence 12 from patent US 6171842
              AR124119
                                                                                                                                                                                                                                                             Bode, W., Engh, R., Hopfner, K.-P., Huber, R. and Kopetzki, E. Chimeric serine proteases
Patent: US 6159722-A 12 12-DEC-2000;
                                                                                                                                                                                                                                                                                                              Unclassified
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7396. .7727
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Pred. No. 1e-21;
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synthetic construct. synthetic construct
                     E36142.1 GI:13022520
JP 1999235173-A/12.
                                                Chimeric serine protease. E36142
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Bode, W., Engh, R., Huber, R., Kopetzki
Chimeric serine proteases
Patent: EP 0927764-A 12 07-JUL-1999;
ROCHE DIAGNOSTICS GMBH (DE)
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Patent: US 6171842-A 12 09-JAN-2001;
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AR124119.1 GI:1'109480
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                               TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 493
                                                     TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
                                                                            GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC
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Patent: JP 199235173-A 12 31-AUG-1999;
ROCHE DIAGNOSTICS GMBH
OS Artificial Sequence
PN JP 199235173-A/12
PD 31-AUG-1999
PF 03-DEC-1997 EP 97121232.9
PI WOLFRAN BODO, RICHARD ENGU, KARL PATER
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Sequence
AR095306
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1 (bases 1 to 725)
Wolfran,B., Richard,E., Karl,P.H., Rolert,H. and Erhard,K.
                                                                                                                                                                                                                                                                         Unclassified.
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C12R1:19)
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Similarity 96.0%;
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Key Location/Qualifiers
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1126)
Leytus, S.P., Chung, D.W., Kisiel, W., Kurachi, K. and Davie, E.W. Characterization of a cDNA coding for human factor x Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3699-3702 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
AR103990
                                                                                                                                                                                                                                                                                                                                                                         In processing, factor X (Stuart factor) is converted to cleavage of a glycopeptide from the amino terminal end o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 to thrombin
                                                                                                                                                                                                                                                                                                                                                                   chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stuart factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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Thorpe, P.E. and Edgington, T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human liver, cDNA to mRNA, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent: US 6093399-A 27 25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methods and compositions for the
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                                                                                                                                                                                                                                                                                                                                                              ge of a glycopeptide from It then acts as a serine
/db_xref="GDB:G00-119-890"
/translation="GFEGKNCELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLA
/translation="GFEGKNCELFTRKLCSLDNGDCDQFCHEEQNSVVCSCARGYTLA
DNGKACIPTGFYPCGKQTLERRKRSVAQATSSSGEAPDSITWKFYDAADLDFTENFFD
                                                                                                                                               /product="factor <1. .1116
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                                                          /protein_id="AAA52486.1"
/db_xref="GI:182821"
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="13q34"
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341 c 342 g
                                                                                             /codon_start=1
                                                                                                            /note="factor X precursor
                                                                                                                                 /gene="F10"
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from patent US 6093399.
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                                                                                                                                                    TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 781
                                                                                                                                                                                                                                                                          95;
coagulation factor X.
Human liver, cDNA to mRNA, clone pKT218.
                                                M22613
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                               M22613.1 GI:180335
                                                          Human blood-coagulation factor x mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
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A93124
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5 bp upstream of TaqI site.
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                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
/db_xref="taxon:32644"
402 c 425 g 22
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AHCLYQAKRFEGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFR
MNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYYDRNSCKLS
SSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGI
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K03194.1 GI:182840 blood coagulation factor; factor x. Human adult liver, cDNA to mRNA, clones pcHX[5,8,14].
                                                                                                    HUMFXM 1443 bp mRNA linear PRI 08-NC Human factor X mRNA, partial signal pept and complete mature
                                                                           K03194
                                                                                                                                                                                                                                                                                                                                                                                                                  h 92.6%;
Similarity 96.0%;
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1 (bases 1 to 1414)

Kaul, R.K., Hildebrand, B., Roberts, S. and Jagadeeswaran, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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//LIANGE TO THE TREQANDI LARVTRANSFLEEMKKGHLERECMEETC
SYEEAREVFED SDKTINEFWIKY KOGDÇCETS PCQNQGKCKDGLGETYTCTCLEGFEGKN
CELFTRKLCSLUNGCLOPGCHEEQNGSVCYCSCARGYTLANDNCKACI PTGPFP-PCGKOTLE
RRKRSVAQATSSGEAPDSITWKPYDAADLDPTENPFDLLDFNQTQPERGDNNITRIV
GGQBCKDGECFWGALLINEENEGFCGGTILLSEFY ILTAAHCLIVAARREFEGDRNTEQEE
GGEAVHEVEVIXHNRFKETYDFDIAVLRIKTPITFERMVAPACLPERDMAESTLMT
OKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSSFITTQNNFCAGYDTKQED
ACCGDSGGPHYTRFKDTYFOTIVSWGEGCARKGKYGIYTKVTAFLKWIDRSMKTRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="coagulation factor X heavy chain"
493. .648
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493. .1401
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/db_xref="GI:180336"
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Pred. No. 1.1e-21;
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  763 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 801
                                                                                          703 GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACTATTC 762
                                               62
                                                                                                                                                                                                      Local
                                                                                                                  2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61
                                             TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fung, M.R., Hay, C.W. and MacGilllvray, R.T.
Characterization of an almost full-length CDNA coding for human blood coagulation factor X
Proc. Natl. Acad. Sci. U.S.A. 82 (11), 3591-3595 (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1985)
2 (bases 3 to 1443)
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                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                    /note="a in pcHx8; t in pcHx5" 361 a 416 c 435 g 231 t bp upstream of Aval site.
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GDB:G00-119-890"
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GREGKNCELFTRKLGSLDNGDCDGFCHBEQNSVVCSCARGYTLADNGKACIPTGPYPC
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NLTRIVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKREKVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPACLPER
DWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSSFIITQNMFC
AGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGESCARKGKYGIYTKVTAFLKWI
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/db_xref="GI:182841"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="factor X signal peptide"
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                                                                                                                                                                                                      91.0%;
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Pred. No. 3.9e-21;
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RESULT 14
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TITLE
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Best Local Similarity 94.9%;
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                                                                                                                                                i (bases 1 to 1467)
Himmelspach,M. and Eibl,J.

FACTOR X ANALOGUES WITH A MODIFIED PROTEASE CLEAVAGE SITE
PATENT: WO 9838317-A 26 03-SEP-1998;
HIMMELSPACH MICHELE (AT); EIBL JOHANN (AT)
                                                                                                                                                                                                                                                                                                                                              1467 bp
Sequence 26 from Patent WO9838317.
A86886
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Falkner,F. and Himmelspach,M.
FACTOR X DELETION MUTANTS AND ANALOGUES THEREOF
PATENT: WO 9838318-A 43 03-SEP-1998;
FALKNER FALKO GUENTER (AT); HIMMELSPACH MICHELE (AT)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                      unidentified
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CLYQAKRFKVRYGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDLAVLRLKTPITF
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IYTKYTAFLKWIDRSMKTRGLPKAKSHAPEVITSSPLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"MCRPLHLVLLSASLAGLLLLGESLFIRREQAUNILARVTRANSF
LEEMKKGHLERECMEETCSYEAREVFEDSDKTNEFWNIKYCGETSPCQNGKCK
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GKACIPTGPYPCGKQTLERRKRSVAQATSSSGEAPDSITWKPYDAADLDPTENPFDLL
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                                                                                                                    Location/Qualifiers
1. .1467
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Pred. No. 3.9e-21;
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SSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFGIVSWGESCARKGKYG
ITYKVTAFLKMIDRSMKTRGLFAKAKSHAPEVITSSPLK*
4 24 c 444 g 236 t

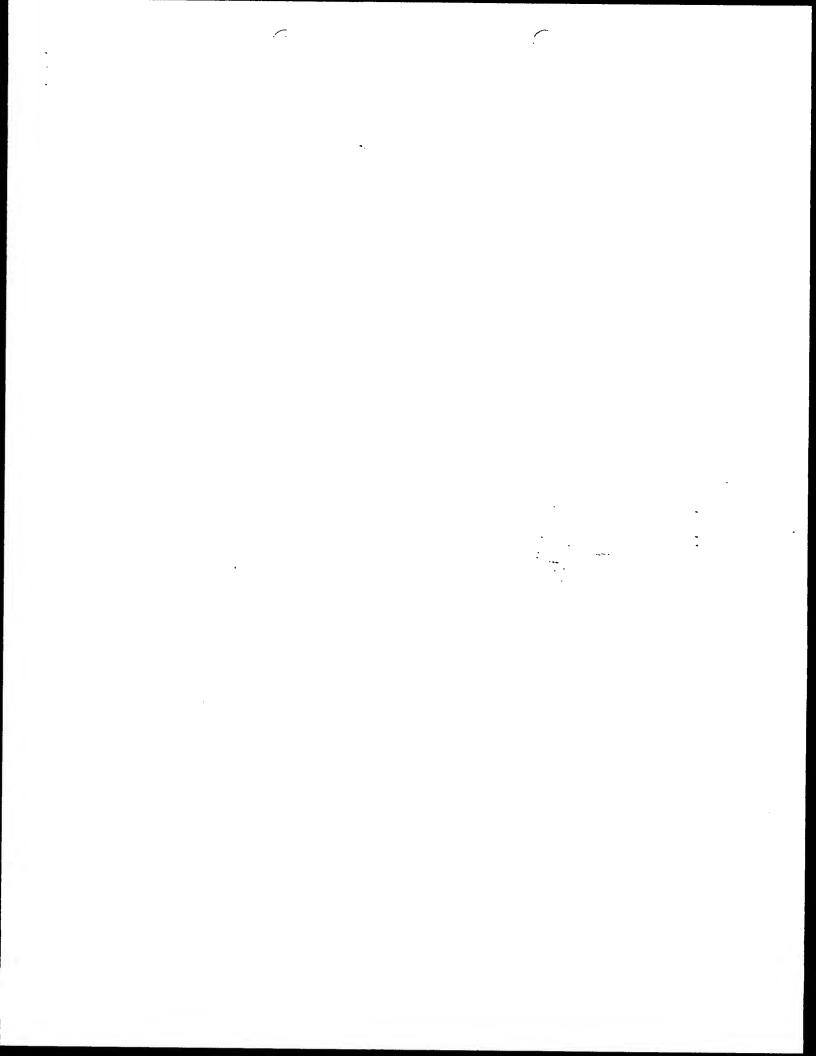
BASE COUNT ORIGIN 363 a

Query Match 91.0%; Best Local Similarity 94.9%; Matches 94; Conservative Score 91; DB 6; Length 1467; pred. No. 3.9e-21; 0; Mismatches 5; Indels

Gaps 0;

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Search completed: January 15, 2003, 20:35:36 Job time: 1354 secs



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Maximum DB seq length: 20
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                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length: 20000000000
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1491.390 Million cell updates/sec
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Listing first 45 summaries
                                                                                                                                                                                                               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
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| _ | 100 | 100.0 | | 21 | AAC70863 | Single nucleotide |
| N | 99.6 | 99.6 | 236 | 21 | AAC70866 | Single nucleotide |
| w | 92.6 | 92.6 | | 20 | AAX78022 | Chimeric serine pr |
| 4 | 92.6 | 92.6 | | 20 | AAX15427 | DNA encoding coagu |
| G | 92.6 | 92.6 | | 21 | AAA89786 | DNA encoding coagu |
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| 32 | | | 3.0 | 3 4 |) (d | | ٠ | 34.2 | | • | | ٠ | • | ٠ | 34.2 | 34.2 | 34.2 | 34.2 | • | • | • | 34.2 | 34.4 | 34.4 | 34.4 | 36 | 63.4 | 75.2 | 91 | 91 | 91 | 91 | 91 | 92.6 |
| | • | | • | • | • | | ٠ | ٠ | • | | ٠ | ٠ | | 34.2 | 34.2 | 34.2 | 34.2 | 34.2 | 34.2 | 34.2 | 34.2 | 34.2 | 34.4 | 34.4 | 34.4 | 36.0 | • | 75.2 | 91.0 | 91.0 | 91.0 | 91.0 | 91.0 | 92.6 |
| 864 | 0 0 | 101 | 713/ | OBI | 2864 | 804 | 2121 | 2081 | 2079 | 2079 | 2063 | 2063 | 2063 | 2063 | 2063 | 2038 | 1854 | 1795 | 1479 | 1305 | 1189 | 699 | 9594 | 3250 | 1250 | 1028 | 1554 | 591 | 1887 | 1507 | 1467 | 1467 | 1467 | 1860 |
| 22 | 1 2 | 3 6 | 2 | 21 | 23 | 23 | 24 | 24 | 24 | 22 | 24 | 22 | 22 | 22 | 21 | 20 | 22 | 22 | 22 | 22 | 24 | 18 | 23 | 23 | 23 | 21 | 15 | 24 | 22 | 21 | 2 | . 19 | 19 | 22 |
| AAC90884 | ABL/1789 | ABL04003 | AAD13114 | AAZ89010 | ABL28900 | ABL28901 | AA164284 | AAI72976 | AAI72975 | AAD13169 | ABK11090 | AAF54396 | AAF92113 | AAS46089 | AAA37099 | AAX87154 | AAH99574 | AAS26880 | AAD02557 | AAD02556 | AAI64290 | AAT79127 | ABL13694 | ABL12390 | ABL12391 | AAA61561 | AAQ71243 | ABK30368 | AAH57469 | AAA54031 | AAF59409 | AAV56821 | AAV56776 | AAF24738 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Flea serine protea | Drosophila melanog | Drosophila melanog | Human membrane-typ | Cavea sp. Factor I | Drosophila melanoq | Drosophila melanog | _ | | a | Human transmembran | cDNA encoding tumo | 5 | | DNA enco | | | | | Human seripancrin | Human seripancrin | Protease D-G catav | | Drosophila melanog | Drosophila melanog | Drosophila melanog | coding mo | ₼ . | | liver ce | factor X | factor x | | ¥, | Nucleotide segment |

ALIGNMENTS

RESULT 1

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WPI; 2000-611722/58.
                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibil(t]; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
                           Altshuler D, Cargill M, Daley GQ,
Lipshutz RJ, Patil N, Sklar P;
                                                                                            31-MAR-1999; 99US-0127248.
                                                                                                                                                                                                                                                      Single nucleotide polymorphism containing sequence #231.
                                                                                                                                                                                                                                                                                                                          AAC70863 standard; DNA; 236 BP.
                                                             (WHED ) WHITEHEAD INST BIOMEDICAL RES. (AFFY-) AFFYMETRIX INC.
                                                                                                                    30-MAR-2000; 2000WO-US08440.
                                                                                                                                            05-CCT-2000.
                                                                                                                                                                   WO200058519-A2
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                             09-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                       AAC70863;
                                     Ireland JS,
                                      Lander ES;
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                                                                                                                                                                                                                                                                                                                                                  (WHED )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; ds.
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                                                                               Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to are useful for phenotypic correlations, forensics, paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC70866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases
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Claim
                                                          medicine and genetic analysis -
                                                                                                                                                                                                                                                          Lipshutz RJ,
                                                                                                                                                                                                                                                                                        Altshuler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200058519-A2
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1;
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                                                                                                                                                                                                                                                                                                                                                  AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                 WHITEHEAD INST
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ilarity 100.0%;
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                                                                                                                                                                                                                                                             Cargill M,
Patil N,
                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127248.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphism containing sequence #232.
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                                                                                                                                                                                                                                                                                        Daley GQ,
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Pred. No. 1.1e-25;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological s, stems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric serine protease FXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-1999
                                                                                                                                                                                                                                                                      03-DEC-1997;
                                                                                                                                                                                                                                                                                                                       07-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                  FXT; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX78022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX78022 standard;
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                                                                                                                                                                              P-PSDB; AAY08894.
                                                                                                                                                                                                                   Bode W,
                                                                                                                                                                                                                                                                                               27-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                            structure; crystallization; haematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.6%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                        antithrombotic; modulator; drug design;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                   Huber R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 G; 47 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                   Kopetzki E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6e-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                             cascade;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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This invention describes a novel chimeric serine protease compound which has antithrombotic activity and comprises two domains with a beta-sheet structure. The first domain corresponds to the first domain of a first serine protease and the second domain corresponds to the second domain of a second serine protease. The products of the invention can be used for identifying antithrombotic agents by determining whether an agent modulates the activity of the serine protease. They can also be used to

identify agents through rational drug

design using information based on

Chimeric

domains, useful

serine protease comprising Factor X and Trypsin useful for identifying thrombolytic agents

catalytic

Example

2; Fig 2; 23pp;

German.

for

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TRESULT 4
AXX15427
ID AXX15427
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Best Local S
Matches 95
The present sequence encodes a coagulation factor. The specification describes tissue factor binding ligands which comprise a binding region which binds to vasculature, particularly of tumours, and a tissue factor construct. The binding ligands can be used for stimulating coagulation in disease-associated vasculature, particularly for the treatment of tumours. The products can also be used for treating e.g. benign prostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
05-MAR-1992;
02-MAR-1994;
11-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCRI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease-associated vasculature; tumour; benign prostatic hyperplasia; diabetic-retinopathy; vascular restenosis; arteriovenous malformation; AVM; meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis; dermatitis; endometriosis; angiofibroma; rheumatoid arthritis; atheroscelotic plaque; corneal graft neovascularisation; haemophilic joint; hypertrophic scar; Osler-Weber syndrome; pyogenic granuloma retrolental fibroplasia; sclerderma; trachoma;
                                                                                                                                                                                                                                                                                            Tissue factor binding ligands - comprising which binds to vasculature, particularly of
                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-189722/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Edgington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5877289-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular adhesion; coagulation factor; factor X/Xa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Truncated tissue factor; tissue factor binding ligand; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding coagulation factor X/Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX15427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX15427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unlike prior art agents are extremely specific for only one factor in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-D crystal structure. The chimeric serine protease, is very good crystallization and for determining structural data and is also ful for the identification of specific antithrombotic agents that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCRIPPS RES
UNIV TEXAS S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TS,
                                                                                                                                                                                                            Columns 129-132; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0479733.
92US-0846349.
94US-0205330.
94US-0273567.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Thorpe PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0479733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INST
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Pred. No. 6.6e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 T; 0 other;
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                                                                                                                                                                                                                                                                                      first binding region tumours, and tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue factor protein; truncated tissue factor; tTF; cytostatic; coagulant; diabetic retinopathy; arteriovenous malformation; meningioma; hemangioma; neovascular glaucoma; psoriasis; synovitis; endometriosis; hemophylic joint; hypertrophic scar; vascular adhesion; tumour; cancer; ligand; human; factor X; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperplasia, diabetic-retinopathy, vascular restenosis, arteriovenous malformations (AVM), meningioma, hemangioma, neovascular glaucoma, psoriasis, synovitis, dermatitis, endometriosis, anglofibroma, rheumatoid arthritis, atheroscelotic plaques, corneal graft neovascularisation, haemophilic joints, hypertrophic scars, Osler-Weber syndrome, pyogenic granuloma retrolental fibroplasia, scleroderma, trachoma, or vascular adhesions. The products can also be used in binding assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding coagulation factor x/Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA89786 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽₽
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1126;
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05-MAR-1992; 02-MAR-1994; 07-JUN-1995; Homo sapiens (TEXA 25-JUL-2000.) SCRIE SCRIPPS RES INST TEXAS 94US-0205330. 94US-0273567. 95US-0482369 92US-0846349 SYSTEM.

WPI; 2000-531471/48

New immunological and growth factor-based bispecific binding ligands, useful for stimulating coagulation in vasculature-associated diseases e.g. for treating both benign and malignant diseases (e.g. meningioma or hemangioma)

Example 9; Column 129-130; 83pp; English.

The present invention relates to a binding ligand with a first binding region that is operatively linked to either a coagulation factor or a second binding region that binds to a coagulation factor. The first binding region binds to a component on the surface of a tumour. The second binding region is all or part of an antibody. An example of a coagulation factor for use in the invention is human truncated tissue factor. Truncated tissue factor (tTF) is the extracellular domain of the protein (see AAB15019). The binding ligand of the

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RESULT 6
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Best Local 9
                              The invention relates to the induction of blood coagulation specifically within tumour vasculature. This is achieved by the use of a bispecific molecule, which comprises a region capable of binding to intratumoral vascular or stromal cells linked to a coagulation factor or to a region capable of binding to a coagulation factor. An example of such a region capable of binding to a coagulation factor. An example of such a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1992;
02-MAR-1994;
11-JUL-1994;
                                                                                                                                                                                                                                                                                                 Kit for inducing coagulation in tumor vasculature, useful for treating malignant or benign growths, contains ligand, linked to coagulation agent, that targets tumor marker \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truncated tissue factor; tTF; human; blood coagulation; tumour vasculature; bispecific antibody; targetting; cancer; vascularised tumour; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention is useful for stimulating coagulation in vasculature associated diseases. Particularly, the binding ligand is useful for treating both benign and malignant diseases that have a vascular component. These diseases include benign growths (e.g. pBH), diabetic retinopathy, arteriovenous malformations, meningioma, hemangioma, neovascular glaucoma, psoriasis, synovitis, endometriosis, hemophylic joints, hypertrophic scars or vascular adhesions. The present binding ligands offer the advantage that even limited damage to the tumour vasculature could produce an avalanche of tumour cell death because each capillary provides oxygen and nutrients for thousands of tumour cells. The present sequence is DNA encoding coagulation factor X/Xa. This factor was used in the invention.
          bispecific molecule is a bispecific
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-269871/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edgington TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCRI ) SCRIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding Factor X/Xa, SEQ ID NO:27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA12970 standard; DNA; 1126 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1126 BP; 269 A; 341 C; 342 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
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                                                                                                                                                                                                                                    Columns 131-132; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEXAS SYSTEM.
PPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0846349.
94US-0205330.
94US-0273567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thorpe PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0479727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
antibody, where one arm binds a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc tumour antigen, and the other arm binds a coagulation factor. The cc expression of certain proteins (tumour antigens) is upregulated in tumour vasculature; such proteins include vascular endothelial growth cc factor (VEGF) and members of the fibroblast growth factor (FGF) family. Cc An antibody or antibody fragment against VEGF or basic FGF (bFGF) may be incorporated into the bispecific molecule in order to target coagulation to tumour vasculature. The coagulation factor-binding portion of the Cc Alfald88) which lacks the cytoplasmic and transmembrane domains. Cc Although tTF can associate with Factor VIIa, the tTF/Factor VIIa complex cannot alone initiate the coagulation cascade as the complex has to be associated with a phospholipid surface for coagulation to occur. Cc However, binding of tTF to tumour vasculature via a tumour antigen/tTF complexed to the initiation of coagulation. Kits for the induction of tumour vasculature via a tumour antigen/tTF complexed to benign diseases associated with a vasculation may be used to treat malignant componiant to be a complex benign growths, prostatic hypertrophy, restenosis, psoriasis, glaucoma, rheumatoid arthritis. Coagulation is induced coagulation to be effective against many different types of cancer. Cc sequences AAA1291-31-AAA12952, AAA12954-A12933 and AAA1297-A12972 cc represent pCR primers used in exemplifications of the present invention to generate constructs encoding tTF, tTF variants or tTF dimers.
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Best Local
                                                                                                         05-MAR-1992;
02-MAR-1994;
                                                                                                                                                                                                                                                                                                                             Vitamin-K dependent coagulation factor; tumour associated vasculature; carcinoma; benign prostatic hyperplasia; diabetic retinopathy; vascular restenosis; arteriovenous malformation; meningoma; haemangiom neovascular glaucoma; psoriasis; cytostatic; antidiabetic; vasotropic;
                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                           US6004555-A
                                                                                                                                                                                                                                                                                                               ophthalmological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                         Vitamin-K-dependent coagulation factor X/Xa coding sequence.
                           (TEXA ) UNIV TEXAS SYSTEM
                                               (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                       21-DEC-1999
                                                                                                                                                                                                                                                                                 Unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal Similarity
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                                                                                       94US-0273567
                                                                                                       92US-0846349.
94US-0205330.
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96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                               Factor X/Xa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1126;
                                                                                                                                                                                                                                                                                                                                                 haemangioma;
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RESULT 8
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AC AAV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                             Factor X; factor IX; serine protease activity; catalytic domain; ZAD; zymogen-activating domain; epidermal growth factor-like domain; EGF1; EGF2; regulator; coagulation; fibrinolysis; homeostasis; X-ray structure; detection; drug modelling; restriction protease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the coding sequence for Factor X/Xa, a vitamin-K-dependent coagulation factor. This coagulation factor can be used in the formation of coagulation factor with the formation of coagulagands. Mutated versions of this sequence can be used in the method for delivering a coagulant to a tumour-associated vasculature using bispecific binding ligands which promote blood coagulation. The binding ligand consists of a binding region that binds to a surface-expressed, surface accessible or surface-localised component of tumour cell, intratumoural vasculature or tumour associated strong. The binding region that the component of tumour cells intratumoural vasculature or tumour associated strong. The
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Factor X protease cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bispecific binding ligands for promoting blood coagulation in a tumour associated vasculature are useful for treating cancer -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease or specific tumour type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-072047/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.6%;
96.0%;
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Pred. No. 7.5e-23;
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Protein production; food processing; protein antiblotic; feed enzyme; protein L; CBD cex protein; cell signal peptide; ss.
                                                                                             Nucleotide sequence of Sig/CBD cex/ER retaining peptide fusion.
                                                                                                                                                                                                                                                                                                    AAF24735 standard; DNA; 1560 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zymogen-activating domain (ZAD), N-terminally bound to an EGF1 and/or EGF2 domain (EGF - epidermal growth factor-like domain). Such proteins are used to identify activators/inhibitors of factor IX family proteins (potentially useful as regulators of coagulation, fibrinolysis and homeostasis). The protein in zymogen form is also useful in assays for detecting factor IXa activity in aqueous solution (specifically in body fluids). The protein can be used to produce co-crystals with protease variants or inhibitors for X-ray structural analysis and drug modelling and as restriction proteases in biotechnology. These truncated proteins have the same specificity as factor IX family proteases and can be produced in prokaryotes in a form that allows production of active enzymby conversion to native form and enzymatic cleavage.
                                                                                                                                                                                20-APR-2001
                                                                                                                                                                                                                                               AAF24735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1404 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the construction of a novel non-glycosylated protein and truncated and zymogen forms of this protein, which have serine protease activity. The protein is composed of various domains from a factor IX family protein, namely a catalytic domain (CD) N-terminally bound to a support of the protein control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-glycosylated, truncated forms of factor IX family protein with serine protease activity - used to screen for specific modulators and to assay factor IXa
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11-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence encodes a human factor X protease. This protein is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96EP-0110959.
96EP-0109288.
96EP-0110109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-EP03027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product- Factor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 A; 404 C; 423 G; 221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "partial coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92.6; DB 19; Length Pred. No. 8.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of active enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 10
AAF24738
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XEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    such as in the food processing industry, e.g. glucoamylases and glucose, isomerases are used for converting starch to high fructose corn syrup, proteinases for the hydrolysis of high molecular weight proteins and in manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipases for cleaving ester linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in healing processes, and to produce animal feed enzymes. The present sequence encodes a fusion protein of the invention, and comprises a fusion of a cell signal peptide, Sig (not specified), CBD cex, and an endoplasmic reticulum retaining peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressing and isolating recombinant protein in a plant, useful for producing large quantities of recombinant proteins, by expressing fusion protein including a cellulose binding peptide fused to a recombinant protein .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                            AAF24738 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein including the recombinant protein and a cellulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, and be a sixth food according to detail to the food according to the combinant proteins and cost-effective manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1560 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for expressing and isolating a recombinant protein in a plant. The method comprising expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 3a; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB31373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shani 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YISS) YISSUM RES DEV CO HEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2000; 2000WO-IL00330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-2000
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                                                     20-APR-2001
                                                                                                                                                                                                                                                                                              837
                                                                                                                                                                                                                     897 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 935
                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                          GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC
                                                                                                                                                                                                                                                                                                                              GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAAACGAGGGTTTCTGTGGTGGAACCATTC 61
                                                                                                                                                                                                                                                        TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-112219/12.
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoseyov O;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0329234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 20..1549
                                                                                                                                                                                                                                                                                                                                                                                                                                         336 A; 479
                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                  92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CO HEBREW UNIV JERUSALEM
                                                                                                                            1860
                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                Score 92.6; DB 22
Pred. No. 8.3e-23;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 454 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                       291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 1560;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                            896
                                                                                                                                                                                                                                                                                                                                                                  0;
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Nucleotide sequence of Sig/CBD-Tma/ER retaining peptide fusion.

RESULT 11
AAV56776
ID AAV56
XX
AC AAV56
XX

AAV56776 standard; DNA; 1467 BP

AAV56776;

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62

TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100

1101

GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 1160 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61

N

Query Match Best Local S Matches 95

Similarity

92.6%;

Score 92.6; DB 22; Pred. No. 8.8e-23; Mismatches

Length 1860; Indels

Conservative

0;

4.

0;

Gaps

0

Sequence 1860 BP; 476 A; 516 C; 555 G; 313 T; 0 other;

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1161

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a recombinant protein in a plant. The method comprising expressing a fusion protein including the recombinant protein and a cellulose binding peptide fused to it, where the fusion protein is compartmentalised and sequestered within plant cells, plant derived tissue or cultured plant cells. The method is useful for obtaining large quantities of the recombinant proteins and protein products in a simple and cost-effective manner. Recombinant proteins may be used commercially, such as in the food processing industry, e.g. glucoamylases and glucose isomerases are used for converting starch to high fructose corn syrup, proteinases for the hydrolysis of high molecular weight proteins and in manufacturing leather or alcoholic beverages, pectinesterases for pectin hydrolysis in food industry, lipases for cleaving ester linkage in triglycerides, and for effluent treatment. The recombinant proteins may further be used to produce protein antibiotics, which can be used in healing processes, and to produce antimal feed enzymes. The present sequence encodes a fusion protein of the invention, and comprises a fusion of a cell signal peptide, Sig (not specified), CBD-Tma, and an endoplasmic reticulum retaining peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressing and isolating recombinant protein in a plant, useful for producing large quantities of recombinant proteins, by expressing a fusion protein including a cellulose binding peptide fused to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein production; food processing; protein antibiotic; protein L; CBD cex protein; cell signal peptide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 4a; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shani Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-2000; 2000WO-IL00330
                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for expressing and isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CBDT-) CBD TECHNOLOGIES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200077174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-112219/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoseyov 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0329234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 20..1873
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27-NOV-1998

(first entry)

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                                                                                                                                                                                                                     method resulting in the production of novel human Factor X (F10)

Canalogues. Such analogues have in the region of the natural F10a

cactivation cleavage site, a modification that creates a processing site

Caron be used to generate, in vivo or in vitro, F10a analogues that

can be used to control bleeding and for treating defects of factors IX.

CVI or VIII, e.g. in hamophiliacs who have developed antibodies to

cactivation is ame conditions. The analogues have high stability and can

be activated without use of animal enzymes such as trypsin. Only

activated without use of animal enzymes such as trypsin. Only

cactivation is affected, their activity is the same as the natural factor.

The analogues can be isolated as a pure single-chain pro-protein (not

cusually possible because of rapid processing of the native precursor) and

this converted to two-chain form by subsequent activation. Activated

canalogues have good stability and structural integrity and are

practically free of inactive intermediates and autoproteolytic
                                                                                                                       Matches
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New factor X analogues with processing site for protease not active on natural protein - and related DNA, is very stable and can be activated in vitro or in vivo without using animal protease(s), particularly for treating disorders of blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes the human Factor X protein which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig 1; 86pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1998
                                                                                                                                                                                 Sequence 1467 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dorner F, Eibl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9838317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Factor X genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONDMMI (OMMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                           737
797
                            62
                                                                                                                                     Local
                                                                         2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61
               TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-481211/41.
DB; AAW76216.
TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 835
                                                           GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACTATTC
                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΙX;
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analogue; activation cleavage site; protease; bleeding;
; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AT-0000335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-AT00045
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121..1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Factor X"
1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                 363 A; 424 C; 444 G;
                                                                                                                                   91.0%;
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                                                                                                                       0;
                                                                                                                                  Score 91; DB 19;
Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Himmelspach
                                                                                                                     Mismatches
                                                                                                                                                                                 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlokat U;
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                                                                                                                                                 Length 1467;
                                                                                                                     Indels
                                                                                                                     0
                                                                                                                  Gaps
                                                           796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human;
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ARESULT 12
AAV56821
ID AAV56
XX AAV56
XX AAV56
XX AAV56
XX Encto
XX Facto
                                This sequence encodes the human Factor X protein which is used in a CC method resulting in the production of novel human Factor X (F10) CC analogues. Such analogues have in the region of the natural F10a CC activation cleavage site, a modification that creates a processing site for a protease that does not naturally cleave F10 in this region. The CC proteins are used to generate, in vivo or in vitro, F10a analogues that CC can be used to control bleeding and for treating defects of factors IX, CC vII or vIII, e.g. in haemophiliacs who have developed antibodies to CC factors VIII and/or IX. The encoding nucleic acid can be used in gene CC therapy of the same conditions. The analogues have high stability and can be activated without use of animal enzymes such as trypsin. Only CC The analogues can be isolated as a pure single-chain pro-protein (not usually possible because of rapid processing of the native precursor) and this converted to two-chain form by subsequent activation. Activated analogues have good stability and structural integrity and are practically free of inactive intermediates and autoproteolytic
                                                                                                                                                                                                                                                                                                                                                                                          New factor 10 deletion mutants lacking the natural protease processing site - but having a non-natural site inserted, and related DNA, particularly for in vitro activation to products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Factor
Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV56821;
                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 1; 82pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW76218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-481212/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Factor X genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV56821 standard; DNA; 1467
                           decomposition products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlokat U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dorner F, Eibl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9838318-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                                                                              to treat blood coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMO ) IMMUNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X; analogue; activation cleavage site; protease; bleeding; human;
IX; Factor VII; Factor VIII; haemophilia; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97AT-0000336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-AT00046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- b
121..1464
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1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Falkner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Factor X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himmelspach M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfleiderer M;
                                                                                                                                                                                                                                                                                                                                                                                              used
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Query Match Matches 94;

Local Similarity

91.0%;

Score 91; DB 19 Pred. No. 3e-22;

Length 1467; other;

Indels

0

Gaps

0

Conservative

0

Mismatches

Sequence 1467

BP; 363 A; 424 C; 444 G;

236 T; 0 19; ú

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                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                       The present invention describes a factor X analogue (I) which contains a modification between Glu226 and Ile235, relative to the 488 residue amino acid sequence given in AAB70411. (I) has haemostatic activity and can be used in gene therapy. (I) encoding pol)...cleotide (II) can be used to produce a drug, which is useful for treatment of patients with blood coagulation disorders, such as patients suffering from haemophiliae, or haemophiliaes with inhibitory antibodies. Preparations containing a polypeptide with factor X/Xa activity are more readily activated by factor Xla or its derivative, which has high stability, without having to use one of the proteases used in prior art to activate the natural factor X, particularly one of animal origins, such as Russell's viper venom (RVV) or trypsin. The present sequence encodes human factor X, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel factor X analog useful for producing drug which is useful for treatment of blood coagulation disorders, such as hemophilia, contains modification between amino acids Glu226 and Ile235 -
                                                                                                                                                                                                                         Sequence 1467 BP; 363 A; 424 C; 444 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blood coagulation disorder; haemophiliac; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human factor X nucleotide sequence SEQ ID NO:1
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797
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                              62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
                                                                                                          2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61
                                                                        GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACTATTC 796
TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTC 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor X; mutant; haemostatic; gene therapy; haemophilia;
                                                                                                                                                                    Similarity
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                                                                                                                                                                91.0%; Score 91; DB 22; Length 1467; 94.9%; Pred. No. 3e-22;
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2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 61

0; Mismatches

0 Gaps

3e-22;

DB 21; Length 1507; 5; Indels

Matches

Similarity

91.0%; Score 91; 94.9%; Pred. No.

Conservative

Sequence 1507 BP; 394 A; 429 C; 446 G; 238 T; 0 other;

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C aspartic acid in the first epidermal growth factor (EGF) domain to C Beta-hydroxyaspartic acid; addition of N- and O-linked C oligosaccharides to the activation peptide; removal of an internal C tripeptide to yield two-chain factor X and removal of the C propeptide just prior to secretion. While some of these modifications CC do not appear essential for factor X function the removal of the C signal sequence, propeptide, internal tripeptide and full C gamma-carboxylation are all steps which are important requisites for CC polyucleotides are described which encode a propeptide fused to a nucleic acid sequence encoding a vitamin K-dependent protein (VKDP). CC The fusion proteins encoded are vitamin K-dependent protein (VKDP). CC gamma-carboxylation of a VKDP to produce a fully gamma-carboxylated C useful for alleviating a VKDP associated disease. The fusion C constructs result in the production of fully gamma-carboxylated C mature VKDPs, which are biologically active. The fusion constructs result in the production of fully gamma-carboxylated C mature VKDPs, which are biologically active. The fusion constructs result in the production of fully gamma-carboxylated C mature VKDPs, which are biologically active. The invention C constructs result in the production of fully gamma-carboxylated C mature protein sequence of human Factor X.
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AAA54031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric DNA for optimizing gamma carboxylation of vitamin K-dependent protein useful for treating diseases associated with the protein, comprises sequence encoding propeptide fused to sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein; fusion protein; coagulation factor; Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues, to gamma-carboxyglutamic acid; modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 6a; 60pp; English.
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AAH57469
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                                                                                                                                                                                                                    CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide' CC sequences (I). (I) can have cytostatic, immunomodulatory and concerning concerning (II) encoded by then are used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening commentics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and CC pharmaceutical agents. Expression of (I) in a sample indicates the CC differentiation of embryonic stem cells into a tissue selected from CC tissues. (I) and (II) are used to produce an expression profile that CC disease or disorder. The gene profile can be used for diagnosis, cc prognosis or monitoring of treatments and for investigating a CC predisposition to a disorder where the gene is associated with a CC cancer, immunopathology or neuropathology.
                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                    Sequence 1887 BP; 467 A; 549 C; 544 G; 327 T; 0 other;
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| cation US/ON: N: Richard Richard Wolfram Wolfram Chimes 20119 ON NUMBER: TE: 2000-0 | ttch 92.6%; Score 92.6; DB 3; Length 725; al Similarity 96.0%; Pred. No. 4e-25; 95; Conservative 0; Mismatches 4; Indels 0; G GTCTGTCACAGGCCCTGCTCAATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC [| fon Erh Erh Karl Hard Fram bert 1999 1998 1998 1998 ens | மைப்பப்ப | 7588 7588 7588 2588 2588 2588 2588 |
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| US/09551028 US/09551028 hard l-Peter d m int ER: US/09/5 i00-04-17 US/09/1 | Score Pred. 0; Mi 0; Mi CAATGAGG | US/09197801B ard -Peter -Peter eric Serine ER: US/09/19 B-11-23 | US-09 US-09 US-09 US-08 PCT-U US-09 | 80 - SD 80 - SD |
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| Proteases 028 | 4e-25 ches ches AACGAGG |)1B | -075A-5 -431-52 -692-52 -613-52 14442A- -101-16 | -906-616-126 -639-075A-12 -012-431-126 -012-63-126 -906-613-126 -485-455D-52 -482-130C-52 -484-211C-52 -906-769-52 -916-769-52 -817-795-52 |
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US/09/197,801

NUMBER OF SEQ ID NOS: PRIOR FILING DATE:

1998-11-23

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; ORGANISM: Homo sapiens
US-09-551-028-12
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SEQ ID NO 12
LENGTH: 725
                                                       Matches
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GENERAL INFORMATION:
                                                                                       Query Match
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Best Local Similarity
                                                                                                                                                                                 TELEX: N/A
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
                                                                                                                                                                                                                                                             NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Specific Coagulation of Vasculature
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/273,567 FILING DATE: 11-JUL-1994
                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: P
SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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2 GTCTGTCACAGGCCCTGCTCATCAATGAGGAAAACGAGGCTTTCTGTGGTGGGAACCATTC 61
                                                                    Local
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5877289
                                                                    Similarity
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                                                       Conservative
                                                                                                                                                                                                                                                   512/474-7577
                                                                                                                                      linear
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                    single
                                                                   92.6%;
96.0%;
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                                                                   Score 92.6; DB 2; Pred. No. 4.79-25;
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                                                       Mismatches
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; Patent No.
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US-08-487-427-27
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
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APPLICANT: Edgington, Thomas S.
APPLICANT: Thorpe, Philip E.
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
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APPLICATION NUMBER: US/08/487,427
FILING DATE: 06-JUN-1995
CLASSIF CATION: 424
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FILING DATE: 11-JUN-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                       455 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 493
                                                                                                                                                                                                                                                                               395 GTCCCTGGCAGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 454
                                                                                                                                                                                                                 62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parker, David L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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5. 6004555
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Sequence 27, Application US/08479727A; Patent No. 6036955

GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
TITLE OF INVENTION: Methods

TITLE OF INVENTION:

Methods and Compositions for the Specific Coagulation of Vasculature

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                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: Edgington, Thomas S.
TITLE OF INVENTION: Methods and Compositions for the Specific TITLE OF INVENTION: Coagulation of Vasculature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versicn #1.30
                    CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/479,727A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                      STATL.
COUNTRY: L.
77210
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                           CITY: Houston
                                                                                                                                                                                                             STREET:
APPLICATION NUMBER: US/08/482,369A
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TELEPHONE: 512/474-7577
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TOPOLOGY: li
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parker, David L. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
95; Conserv
                                                                                                                                                                        Texas
                                                                                                                                                                                                           EE: Arnold, White & Durkee
P.O. Box 4433
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                                                                                                                                                                                                                                                                        Coagulation of Vasculature 32
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US-08-482-369A-27
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      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07439
FILING DATE: Concurrently herewith
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                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                APPLICANT:
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LENGTH: 1126 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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NAME: Parker, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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CLASSIFICATION:
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                                                                                                                                                                 STATE:
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STRANDEDNESS: single
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                                                                                                                                              COUNTRY:
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                                                                                                                                 77210
                                                                                                                                                               Texas
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VENTION: METHODS AND COMPOSITIONS
VENTION: FOR THE SPECIFIC
VENTION: FOR THE SPECIFIC
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STREET: 201
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                                                                                                                                                                                              Box 4433
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                                                                                                                                                                                                                                              COAGULATION OF VASCULATURE 27
                                                                                                                                                                                                                                                                                                                                                                        NO: (512)499-4462
(512)499-4523
(512)499-4523
THE SCRIPPS RESEARCH INSTITUTE
10666 North Torrey Pines Road
                                                                                                                                                                                                              White & Durkee
                                                                                                                                                                                                                                                                                                                           United States of America
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Pred. No. 4.7e-25;
0; Mismatches 4; Indels 0
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Patent No. 5795863

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; MOLECULE TYPE:
US-09-202-101-15
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; Sequence 4, Application US/08487037
                US-08-487-037-4
                                 RESULT 9
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                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
TYPE: single
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1126 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: UTI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (713) 789-2679
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APPLICATION NUMBER: US 08/273,567
FILING DATE: 11-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                        683 GTCCCTGGCAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTC 742
                                                                            743 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 781
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                                                                                                                                                        Match 92.6%;
Local Similarity 96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 100
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                                                                                                                                                                                                          95;
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; NAME/KEY: misc_feature
; LOCATION: (1)..(591)
; OTHER INFORMATION: n = a,
US-09-280-116-138
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                                                                                                                                                       Sequence 138, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
APPLICANT: ROBLSON, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 138
LENGTH: 591
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
                                                                                                                       ORGANISM: Homo sapiens
                                                                            FEATURE:
OTHER INFORMATION: trypsin-like serine proteases
                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1500 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    829 TGAGCGAGTTCTACATCCTAACGGCAGCCCACTGTCTCT 867
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REGISTRATION NUMBER: 30,988
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Pred. No. 2e-24;
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Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                     FEATURE:
                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Improved TITLE OF INVENTION: proteins NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS:
                                                                                                                                                             MOLECULE TYPE: CD
HYPOTHETICAL: YES
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                      NAME/KEY:
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STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                         NAME: Paul T. Clark REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/469,486
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                                                                                                                                                                                                                                                     ENGTH:
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Pred. No. 1.1e-18;
                            Score 63.4; DB 1;
Pred. No. 3.6e-14;
               Mismatches
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                                            DB 1;
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                                        Length 1554;
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                                                                                 Matches
                                                                                                                                                Query Match
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APPLICANT: Thege
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LENGTH: 1554 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BENEFIT COMPATIBLE
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REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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TELLEFAX: 200154
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10 CAGGCCCTGCTCATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCATTCTGAGCGAG 69
                                                                                                           Local
                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/469,658 FILING DATE: June 5, 1995
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                                                                                                           Similarity
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                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark
                                                                                                           63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPROVED METHOD FOR THE REFOLDING OF
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                                                                         0
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                                                                                                           Score 63.4; DB 2;
Pred. No. 3.6e-14;
                                                                         Mismatches
                                                                                                                                            DB 2;
                                                                                                                                        Length 1554;
                                                                         Indels
                                                                      0;
                                                                      Gaps
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817 CAGGCTCTGCTGGTCAACGAAGAGAACGAGGGATTCTGCGGGGGCACCATCCTGAACGAG 876

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RESULT 14
US-09-656-002-1
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-008-271A-18
Sequence 1, Application US/09656002 Patent No. 6455668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application Patent No. 6203979
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             856 CATCCAGTACGACAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCT 915
                                                                                                             916 CACGGCAGCCCACTGCTTC 934
                                                                                                                                               81 AACGGCAGCCCACTGTCTC 99
                                                                                                                                                                                                   21 CATCAATGAGGAAAACGAGGGTTTCTGTGGTGGAACCAT PCTGAGCGAGTTCTACATCC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandman, Olga
Hillman, Jenn:
                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: COLNNOT13
CLONE: 1337018
                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09008271A
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guegler, Karl J. Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang, Tom Y.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                      34.2%; Score 34.2; DB 4; Length 2038; 64.6%; Pred. No. 0.0026; tive 0; Mismatches 28; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jennifer L
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                        Gaps
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APPLICANT: WILSON, Keith
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, ;
TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
FILE REFERENCE: A-65108/DB/JJD/AMS
CURRENT FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US/09/656,002
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 09/525,993
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 09/493,444
PRIOR FILING DATE: 2000-03-15
SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NOS: 3
SOFTWARE: PATENTIN VERSION 3.0
LENGTH: 2079
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŷ
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Patent No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: Mack, David
APPLICANT: Gish, Kurt
APPLICANT: Wilson, Kei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
ATTORNEY JAGENT INFORMATION:
NAME: Connell, Gary J
REGISTRATION NUMBER: 32,020
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                               SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NU
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            931 CACGGCAGCCCACTGCTTC 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        871 CATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCT 930
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AACGGCAGCCCACTGTCTC 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                80203
                                                                                                                                                                                                                                                                                                      f: 1700 Lincoln Street, Suite 3500
Denver
: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38, Application US/08906769
6077687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaines, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frank, Glenn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                           Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%; Score 34.2; DB 4; Length 2079; 64.6%; Pred. No. 0.0027;
                                                                                                                                                                           Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                        190
                                                                                                                                              us/08/906,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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REFERENCE/DOCKET NUMBER: 2618-25-C2

TELECHONE (303) 863-9700

TELEPHONE: (303) 863-9700

INFORMATION FOR SED ID NO: 138:

SEQUENCE CHARACTERISTICS:

LENCYH: 864 base pairs

TYPE: nucleic cald

TYPE: nucleic cald

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDN

FEATURE:

LOCATION: 2.781

COTHER INFORMATION: K; at pos. bp 456, change G to
OTHER INFORMATION: Substitute Xaa.*

OTHER INFORMATION: Substitute Xaa.*

OTHER INFORMATION: Substitute Xaa.*

OUTHER INFORMATION: Subst
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